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(71) Applicant *(for all designated States except US)*: **BIONOMICS LIMITED** [AU/AU]; 31 Dalgleish Street, Thebarton, South Australia 5031 (AU).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **GONDA, Thomas, John** [AU/AU]; 10 Halimah Street, Chapel Hill, Queensland 4069 (AU). **KREMMIDIOTIS, Gabriel** [AU/AU]; 49 Sturt Approach, Flagstaff Hill, South Australia 5159 (AU).

(74) Agent: **GRIFFITH HACK**; G P O Box 3125, Level 10, 167 Eagle Street, Brisbane, Queensland 4001 (AU).

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(54) Title: METHOD FOR IDENTIFYING NUCLEIC ACID MOLECULES ASSOCIATED WITH ANGIOGENESIS

(57) Abstract: A method for the identification of a nucleic acid molecule differentially expressed in an in vitro model of a biological system, comprising the steps of: (1) harvesting cells from the model system at predetermined time points; (2) obtaining total RNA from the cells harvested at each time point; (3) preparing cDNA from the total RNA from each time point to provide a plurality of pools of cDNA; (4) performing a suppression subtractive hybridization (SSH) on the cDNA pools from each time point sequentially so as to progressively amplify cDNAs derived from nucleic acid molecules differentially expressed from one time period to the next.

Method for identifying nucleic acid molecules associated with angiogenesis

Technical Field

The present invention relates to novel nucleic acid sequences ("angiogenic genes") involved in the process of angiogenesis. Each of the angiogenic genes encode a polypeptide that has a role in angiogenesis. In view of the realisation that these genes play a role in angiogenesis, the invention is also concerned with the therapy of pathologies associated with angiogenesis, the screening of drugs for pro- or anti-angiogenic activity, the diagnosis and prognosis of pathologies associated with angiogenesis, and in some cases the use of the nucleic acid sequences to identify and obtain full-length angiogenesis-related genes.

Background Art

The formation of new blood vessels from pre-existing vessels, a process termed angiogenesis, is essential for normal growth. Important angiogenic processes include those taking place in embryogenesis, renewal of the endometrium, formation and growth of the corpus luteum of pregnancy, wound healing and in the restoration of tissue structure and function after injury.

The formation of new capillaries requires a co-ordinated series of events mediated through the expression of multiple genes which may have either pro- or anti-angiogenic activities. The process begins with an angiogenic stimulus to existing vasculature, usually mediated by growth factors such as vascular endothelial growth factor or basic fibroblast growth factor. This is followed by degradation of the extracellular matrix, cell adhesion changes (and disruption), an increase in cell permeability, proliferation of endothelial cells (ECs) and migration of ECs towards the site of blood vessel formation. Subsequent processes include capillary tube or

lumen formation, stabilisation and differentiation by the migrating ECs.

In the (normal) healthy adult, angiogenesis is virtually arrested and occurs only when needed. However, a number of pathological situations are characterised by enhanced, uncontrolled angiogenesis. These conditions include cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis and cardiovascular diseases such as atherosclerosis. In other pathologies such as ischaemic limb disease or in coronary artery disease, growing new vessels through the promotion of an expanding vasculature would be of benefit.

A number of *in vitro* assays have been established which are thought to mimic angiogenesis and these have provided important tools to examine the mechanisms by which the angiogenic process takes place and the genes most likely to be involved.

Lumen formation is a key step in angiogenesis. The presence of vacuoles within ECs undergoing angiogenesis have been reported and their involvement in lumen formation has been postulated (Folkman and Haudenschild, 1980; Gamble et al., 1993). The general mechanism of lumen formation suggested by Folkman and Haudenschild (1980), has been that vacuoles form within the cytoplasm of a number of aligned ECs which are later converted to a tube. The union of adjacent tubes results in the formation of a continuous unicellular capillary lumen. However, little is known about the changes in cell morphology leading to lumen formation or the signals required for ECs to construct this feature.

An *in vitro* model of angiogenesis has been created from human umbilical vein ECs plated onto a 3 dimensional collagen matrix (Gamble et al., 1993). In the presence of phorbol myristate acetate (PMA) these cells form capillary tubes within 24 hours. With the addition of anti-integrin antibodies, the usually unicellular tubes (thought to reflect an immature, poorly differentiated phenotype) are

converted to form a multicellular lumen through the inhibition of cell-matrix interactions and promotion of cell-cell interactions. This model has subsequently allowed the investigation of the morphological events which occur in lumen formation.

For the treatment of diseases associated with angiogenesis, understanding the molecular genetic mechanisms of the process is of paramount importance. The use of the *in vitro* model described above (Gamble et al., 1993), a model that reflects the critical events that occur during angiogenesis *in vivo* in a time dependant and broadly synchronous manner, has provided a tool for the identification of the key genes involved.

Disclosure of the Invention

Total RNA from cells harvested at specific time points from a biological model, in this case the Gamble et al (1993) model for angiogenesis, were used to prepare cDNAs, which were subjected to a novel process incorporating suppression subtractive hybridization (SSH) to identify cDNAs derived from differentially expressed genes.

According to one aspect of the present invention there is provided a method for the identification of a gene differentially expressed in an *in vitro* model of a biological system, comprising the steps of:

(1) harvesting cells from the model system at predetermined time points;

(2) obtaining total RNA from the cells harvested at each time point;

(3) preparing cDNA from the total RNA from each time point to provide a plurality of pools of cDNA;

(4) performing a suppression subtractive hybridization (SSH) on the cDNA pools from each time point sequentially so as to progressively amplify cDNAs derived from genes differentially expressed from one time period to the next.

Thus, up-regulation of a gene whose expression subsequently remains up-regulated at the same level will be detected (and the cDNA amplified) only in the first time period where the level cDNA is elevated, as the quantity of cDNA in pools from the subsequent time points will be the same. This reduction in redundancy reduces the possibility that other genes of lower representation in the cell mRNA expression pool will be masked. In a particularly preferred embodiment of the present invention the model system is an *in vitro* model for angiogenesis (Gamble *et al.*, 1993).

Those cDNAs identified to be differentially expressed in the SSH process were cloned and subjected to microarray analysis, which lead to the identification of a number of genes that are up-regulated in their expression during the angiogenesis process.

According to a further aspect of the present invention there is provided a method for the identification of a gene up-regulated in an *in vitro* model of a biological system, comprising the steps of:

(1) harvesting cells from the model system at predetermined time points;

(2) obtaining total RNA from the cells harvested at each time point;

(3) preparing cDNA from the total RNA from each time point to provide a plurality of pools of cDNA;

(4) performing a suppression subtractive hybridization (SSH) on the cDNA pools from each time point sequentially so as to progressively amplify cDNAs derived from genes differentially expressed from one time period to the next.

(5) cloning the amplified cDNAs;

(6) locating DNA from each clone on a microarray;

(7) generating antisense RNA by reverse transcription of total RNA from cells harvested from the *in vitro* model at said predetermined time intervals and

labelling the antisense RNA; and

(8) probing the microarray with labelled antisense RNA from 0 hours and each of the other time points separately to identify clones containing cDNA derived from genes which are up-regulated at said time points in the *in vitro* model.

Functional analysis of a subset of these up-regulated angiogenic genes and their effect on endothelial cell function and capillary tube formation is described in detail below.

Accordingly, the present invention provides isolated nucleic acid molecules, which have been shown to be up-regulated in their expression during angiogenesis (see Tables 1 and 2). The isolation of these angiogenic genes has provided novel targets for the treatment of angiogenesis-related disorders.

In a first aspect of the present invention there is provided an isolated nucleic acid molecule as defined by SEQ ID Numbers: 1 to 44.

Following the realisation that these molecules, and those listed in Tables 1 and 2, are up-regulated in their expression during angiogenesis, the invention provides isolated nucleic acid molecules as defined by SEQ ID Numbers: 1 to 44, and laid out in Tables 1 and 2, or fragments thereof, that play a role in an angiogenic process. Such a process may include, but is not restricted to, embryogenesis, menstrual cycle, wound repair, tumour angiogenesis and exercise induced muscle hypertrophy.

In addition, the present invention provides isolated nucleic acid molecules as defined by SEQ ID Numbers: 1 to 44, and laid out in Tables 1 and 2 (hereinafter referred to as "angiogenic genes", "angiogenic nucleic acid molecules" or "angiogenic polypeptides" for the sake of convenience), or fragments thereof, that play a role in diseases associated with the angiogenic process. Diseases may include, but are not restricted to, cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis, and

cardiovascular diseases such as atherosclerosis, ischaemic limb disease and coronary artery disease. Useful fragments may include those which are unique and which do not overlap any previously identified genes, unique fragments which do overlap with a known sequence, and fragments which span alternative splice junctions etc.

The invention also encompasses an isolated nucleic acid molecule that is at least 70% identical to any one of the angiogenic genes of the invention and which plays a role in the angiogenic process.

Such variants will have preferably at least about 85%, and most preferably at least about 95% sequence identity to the angiogenic genes. Any one of the polynucleotide variants described above can encode an amino acid sequence, which contains at least one functional or structural characteristic of the relevant angiogenic gene of the invention.

Sequence identity is typically calculated using the BLAST algorithm, described in Altschul *et al* (1997) with the BLOSUM62 default matrix.

The invention also encompasses an isolated nucleic acid molecule which hybridizes under stringent conditions with any one of the angiogenic genes of the invention and which plays a role in an angiogenic process.

Hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, may be used to identify nucleic acid sequences which encode the relevant angiogenic gene. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding the angiogenic gene, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 50%

sequence identity to any of the angiogenic gene-encoding sequences of the invention. The hybridization probes of the present invention may be DNA or RNA and may be derived from any one of the angiogenic gene sequences or from genomic sequences including promoters, enhancers, and introns of the angiogenic genes.

Means for producing specific hybridization probes for DNAs encoding any one of the angiogenic genes include the cloning of polynucleotide sequences encoding the relevant angiogenic gene or its derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, and are commercially available. Hybridization probes may be labelled by radionuclides such as ^{32}P or ^{35}S, or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, or other methods known in the art.

Under stringent conditions, hybridization with ^{32}P labelled probes will most preferably occur at 42°C in 750 mM NaCl, 75 mM trisodium citrate, 2% SDS, 50% formamide, 1X Denhart's, 10% (w/v) dextran sulphate and 100 µg/ml denatured salmon sperm DNA. Useful variations on these conditions will be readily apparent to those skilled in the art. The washing steps which follow hybridization most preferably occur at 65°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

The nucleic acid molecules, or fragments thereof, of the present invention have a nucleotide sequence obtainable from a natural source. They therefore include naturally occurring normal, naturally occurring mutant, naturally occurring polymorphic alleles, differentially spliced transcripts, splice variants etc. Natural sources include animal cells and tissues, body fluids, tissue culture cells etc.

The nucleic acid molecules of the present invention can also be engineered using methods accepted in the art

so as to alter the angiogenic gene-encoding sequences for a variety of purposes. These include, but are not limited to, modification of the cloning, processing, and/or expression of the gene product. PCR reassembly of gene fragments and the use of synthetic oligonucleotides allow the engineering of angiogenic gene nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis can introduce mutations that create new restriction sites, alter glycosylation patterns and produce splice variants etc.

As a result of the degeneracy of the genetic code, a number of nucleic acid sequences encoding the angiogenic genes of the invention, some that may have minimal similarity to the nucleic acid sequences of any known and naturally occurring gene, may be produced. Thus, the invention includes each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of the naturally occurring angiogenic gene, and all such variations are to be considered as being specifically disclosed.

The nucleic acid molecules of this invention are typically DNA molecules, and include cDNA, genomic DNA, synthetic forms, and mixed polymers, both sense and antisense strands, and may be chemically or biochemically modified, or may contain non-natural or derivatised nucleotide bases as will be appreciated by those skilled in the art. Such modifications include labels, methylation, intercalators, alkylators and modified linkages. In some instances it may be advantageous to produce nucleotide sequences encoding an angiogenic gene or its derivatives possessing a substantially different codon usage than that of the naturally occurring gene. For example, codons may be selected to increase the rate of expression of the peptide in a particular prokaryotic or

eukaryotic host corresponding with the frequency that the host utilizes particular codons. Other reasons to alter the nucleotide sequence encoding an angiogenic gene or its derivatives without altering the encoded amino acid sequence include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of the nucleic acid molecules of the invention, entirely by synthetic chemistry. Synthetic sequences may be inserted into expression vectors and cell systems that contain the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements may include regulatory sequences, promoters, 5' and 3' untranslated regions and specific initiation signals (such as an ATG initiation codon and Kozak consensus sequence) which allow more efficient translation of sequences encoding the angiogenic genes. In cases where the complete coding sequence including its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, additional control signals may not be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals as described above should be provided by the vector. Such signals may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used (Scharf et al., 1994).

The invention also includes nucleic acid molecules that are the complements of the sequences described herein.

The present invention allows for the preparation of purified polypeptides or proteins. In order to do this, host cells may be transfected with a nucleic acid molecule as described above. Typically, said host cells are

transfected with an expression vector comprising a nucleic acid molecule according to the invention. A variety of expression vector/host systems may be utilized to contain and express the sequences. These include, but are not limited to, microorganisms such as bacteria transformed with plasmid or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); or mouse or other animal or human tissue cell systems. Mammalian cells can also be used to express a protein that is encoded by a specific angiogenic gene of the invention using various expression vectors including plasmid, cosmid and viral systems such as a vaccinia virus expression system. The invention is not limited by the host cell or vector employed.

The nucleic acid molecules, or variants thereof, of the present invention can be stably expressed in cell lines to allow long term production of recombinant proteins in mammalian systems. Sequences encoding any one of the angiogenic genes of the invention can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. The selectable marker confers resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode a protein may be designed to contain signal sequences which direct secretion of the protein through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its

ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, glycosylation, phosphorylation, and acylation. Post-translational cleavage of a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells having specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO or HeLa cells), are available from the American Type Culture Collection (ATCC) and may be chosen to ensure the correct modification and processing of the foreign protein.

According to still another aspect of the present invention there is provided an expression vector comprising a nucleic acid molecule of the invention as described above.

According to still another aspect of the present invention there is provided a cell comprising a nucleic acid molecule of the invention as described above.

When large quantities of protein are needed such as for antibody production, vectors which direct high levels of expression may be used such as those containing the T5 or T7 inducible bacteriophage promoter. The present invention also includes the use of the expression systems described above in generating and isolating fusion proteins which contain important functional domains of the protein. These fusion proteins are used for binding, structural and functional studies as well as for the generation of appropriate antibodies.

In order to express and purify the protein as a fusion protein, the appropriate polynucleotide sequences of the present invention are inserted into a vector which contains a nucleotide sequence encoding another peptide (for example, glutathionine succinyl transferase). The fusion protein is expressed and recovered from prokaryotic or eukaryotic cells. The fusion protein can then be

purified by affinity chromatography based upon the fusion vector sequence and the relevant protein can subsequently be obtained by enzymatic cleavage of the fusion protein.

Fragments of polypeptides of the present invention may also be produced by direct peptide synthesis using solid-phase techniques. Automated synthesis may be achieved by using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Various fragments of polypeptide may be synthesized separately and then combined to produce the full length molecule.

In instances where the isolated nucleic acid molecules of the invention represent only partial gene sequence, these partial sequences can be used to obtain the corresponding sequence of the full-length angiogenic gene. Therefore, the present invention further provides the use of a partial nucleic acid molecule of the invention comprising a nucleotide sequence defined by any one of SEQ ID Numbers: 1 to 15, 17 to 37, and 39 to 44 to identify and/or obtain full-length human genes involved in the angiogenic process. Full-length angiogenic genes may be cloned using the partial nucleotide sequences of the invention by methods known *per se* to those skilled in the art. For example, *in silico* analysis of sequence databases such as those hosted at the National Centre for Biotechnology Information (http://www.ncbi.nlm.nih.gov/) can be searched in order to obtain overlapping nucleotide sequence. This provides a "walking" strategy towards obtaining the full-length gene sequence. Appropriate databases to search at this site include the expressed sequence tag (EST) database (database of GenBank, EMBL and DDBJ sequences from their EST divisions) or the non redundant (nr) database (contains all GenBank, EMBL, DDBJ and PDB sequences but does not include EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences). Typically searches are performed using the BLAST algorithm described in Altschul *et al* (1997) with the BLOSUM62 default matrix. In instances where *in silico* "walking" approaches fail to

retrieve the complete gene sequence, additional strategies may be employed. These include the use of "restriction-site PCR" will allows the retrieval of unknown sequence adjacent to a portion of DNA whose sequence is known. In this technique universal primers are used to retrieve unknown sequence. Inverse PCR may also be used, in which primers based on the known sequence are designed to amplify adjacent unknown sequences. These upstream sequences may include promoters and regulatory elements. In addition, various other PCR-based techniques may be used, for example a kit available from Clontech (Palo Alto, California) allows for a walking PCR technique, the 5'RACE kit (Gibco-BRL) allows isolation of additional 5' gene sequence, while additional 3' sequence can be obtained using practised techniques (for example see Gecz et al., 1997).

In a further aspect of the present invention there is provided an isolated polypeptide as defined by SEQ ID Numbers: 51 to 58 and laid out in Table 1.

The present invention also provides isolated polypeptides, which have been shown to be up-regulated in their expression during angiogenesis (see Tables 1 and 2).

More specifically, following the realisation that these polypeptides are up-regulated in their expression during angiogenesis, the invention provides isolated polypeptides as defined by SEQ ID Numbers: 51 to 58, and as laid out in Tables 1 and 2, or fragments thereof, that play a role in an angiogenic process. Such a process may include, but is not restricted to, embryogenesis, menstrual cycle, wound repair, tumour angiogenesis and exercise induced muscle hypertrophy.

In addition, the present invention provides isolated polypeptides as defined by SEQ ID Numbers: 51 to 58, and as laid out in Tables 1 and 2, or fragments thereof, that play a role in diseases associated with the angiogenic process. Diseases may include, but are not restricted to, cancer, rheumatoid arthritis, diabetic retinopathy,

psoriasis, and cardiovascular diseases such as atherosclerosis, ischaemic limb disease and coronary artery disease.

The invention also encompasses an isolated polypeptide having at least 70%, preferably 85%, and more preferably 95%, identity to any one of SEQ ID Numbers: 51 to 58, and which plays a role in an angiogenic process.

Sequence identity is typically calculated using the BLAST algorithm, described in Altschul *et al* (1997) with the BLOSUM62 default matrix.

In a further aspect of the invention there is provided a method of preparing a polypeptide as described above, comprising the steps of:

(1) culturing cells as described above under conditions effective for production of the polypeptide; and

(2) harvesting the polypeptide.

According to still another aspect of the invention there is provided a polypeptide which is the product of the process described above.

Substantially purified protein or fragments thereof can then be used in further biochemical analyses to establish secondary and tertiary structure. Such methodology is known in the art and includes, but is not restricted to, X-ray crystallography of crystals of the proteins or by nuclear magnetic resonance (NMR). Determination of structure allows for the rational design of pharmaceuticals to interact with the protein, alter protein charge configuration or charge interaction with other proteins, or to alter its function in the cell.

The invention has provided a number of genes likely to be involved in angiogenesis and therefore enables methods for the modulation of angiogenesis. As angiogenesis is critical in a number of pathological processes, the invention therefore also enables therapeutic methods for the treatment of all angiogenesis-related disorders, and may enable the diagnosis or

prognosis of all angiogenesis-related disorders associated with abnormalities in expression and/or function of any one of the angiogenic genes.

Examples of such disorders include, but are not limited to, cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis, and cardiovascular diseases such as atherosclerosis, ischaemic limb disease and coronary artery disease.

Therapeutic Applications

According to another aspect of the present invention there is provided a method of treating an angiogenesis-related disorder as described above, comprising administering a selective antagonist or agonist of an angiogenic gene or protein of the invention to a subject in need of such treatment.

In still another aspect of the invention there is provided the use of a selective antagonist or agonist of an angiogenic gene or protein of the invention in the manufacture of a medicament for the treatment of an angiogenesis-related disorder as described above.

For the treatment of angiogenesis-related disorders which result in uncontrolled or enhanced angiogenesis, including but not limited to, cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis and cardiovascular diseases such as atherosclerosis, therapies which inhibit the expanding vasculature are desirable. This would involve inhibition of any one of the angiogenic genes or proteins that are able to promote angiogenesis, or enhancement, stimulation or re-activation of any one of the angiogenic genes or proteins that are able to inhibit angiogenesis.

For the treatment of angiogenesis-related disorders which are characterised by inhibited or decreased angiogenesis, including but not limited to, ischaemic limb disease and coronary artery disease, therapies which enhance or promote vascular expansion are desirable. This

would involve inhibition of any one of the angiogenic genes or proteins that are able to restrict angiogenesis or enhancement, stimulation or re-activation of any one of the angiogenic genes or proteins that are able to promote angiogenesis.

For instance, decreasing the expression of BNO782 and BNO481 has been shown to disrupt endothelial cell activity leading to an inhibition of capillary tube formation and angiogenesis. Therefore, in the treatment of disorders where angiogenesis needs to be restricted, it would be desirable to inhibit the function of these genes. Alternatively, in the treatment of disorders where angiogenesis needs to be stimulated it may be desirable to enhance the function of these genes.

For each of these cases, the relevant therapy will be useful in treating angiogenesis-related disorders regardless of whether there is a lesion in the angiogenic gene.

Inhibiting gene or protein function

Inhibiting the function of a gene or protein can be achieved in a variety of ways. Antisense nucleic acid methodologies represent one approach to inactivate genes that are causative of a disorder. Antisense or gene-targeted silencing strategies may include, but are not limited to, the use of antisense oligonucleotides, injection of antisense RNA, transfection of antisense RNA expression vectors, and the use of RNA interference (RNAi) or short interfering RNAs (siRNA). RNAi can be used *in vitro* and *in vivo* to silence a gene when its expression contributes to angiogenesis (Sharp and Zamore, 2000; Grishok et al., 2001). Still further, catalytic nucleic acid molecules such as DNAzymes and ribozymes may be used for gene silencing (Breaker and Joyce, 1994; Haseloff and Gerlach, 1988). These molecules function by cleaving their target mRNA molecule rather than merely binding to it as in traditional antisense approaches.

In one aspect of the invention an isolated nucleic acid molecule, which is the complement of any one of the relevant angiogenic nucleic acid molecules described above may be administered to a subject in need of such treatment. Typically, a complement to any relevant one of the angiogenic genes is administered to a subject to treat or prevent an angiogenesis-related disorder. In a further aspect the complement may encode an RNA molecule that hybridizes with the mRNA encoded by the relevant angiogenic gene of the invention or may be a short interfering oligonucleotide (siRNA) that hybridizes with the mRNA encoded by the relevant angiogenic gene of the invention.

In a further aspect of the invention there is provided the use of an isolated nucleic acid molecule which is the complement of any one of the relevant nucleic acid molecules of the invention and which encodes an RNA molecule or a short interfering oligonucleotide (siRNA) that hybridizes with the mRNA encoded by the relevant angiogenic gene of the invention, in the manufacture of a medicament for the treatment of an angiogenesis-related disorder.

Typically, a vector expressing the complement of a polynucleotide encoding any one of the relevant angiogenic genes may be administered to a subject to treat or prevent an angiogenesis-related disorder including, but not limited to, those described above. Many methods for introducing vectors into cells or tissues are available and equally suitable for use *in vivo*, *in vitro*, and *ex vivo*. For *ex vivo* therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (For example, see Goldman *et al.*, 1997).

In a further aspect purified protein according to the

invention may be used to produce antibodies which specifically bind any relevant angiogenic protein of the invention. These antibodies may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent (such as a cytotoxic agent) to cells or tissues that express the relevant angiogenic protein. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric and single chain antibodies as would be understood by the person skilled in the art.

For the production of antibodies, various hosts including rabbits, rats, goats, mice, humans, and others may be immunized by injection with a protein of the invention or with any fragment or oligopeptide thereof, which has immunogenic properties. Various adjuvants may be used to increase immunological response and include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface-active substances such as lysolecithin. Adjuvants used in humans include BCG (bacilli Calmette-Guerin) and Corynebacterium parvum.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to the relevant angiogenic protein have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of amino acids from these proteins may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to any relevant angiogenic protein may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma

technique, and the EBV-hybridoma technique. (For example, see Kohler and Milstein, 1975; Kozbor et al., 1985; Cote et al., 1983; Cole et al., 1984).

Monoclonal antibodies produced may include, but are not limited to, mouse-derived antibodies, humanised antibodies and fully-human antibodies. For example, antibodies are obtained from transgenic mice that have been engineered to produce specific human antibodies in response to antigenic challenge. In one example of this technique, elements of the human heavy and light chain loci are introduced into strains of mice derived from embryonic stem cell lines that contain targeted disruptions of the endogenous heavy and light chain loci. These transgenic mice can synthesise human antibodies specific for human antigens and can be used to produce human antibody-secreting hybridomas. Methods for obtaining human antibodies from transgenic mice are described for example in Lonberg et al., 1994; Green et al., 1994; Taylor et al., 1994.

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (For example, see Orlandi et al., 1989; Winter et al., 1991).

Antibody fragments which contain specific binding sites for any relevant angiogenic protein may also be generated. For example, such fragments include, F(ab')2 fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')2 fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (For example, see Huse et al., 1989).

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or

immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between a protein and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes is preferred, but a competitive binding assay may also be employed.

In a further aspect, antagonists may include peptides, phosphopeptides or small organic or inorganic compounds. These antagonists should disrupt the function of any relevant angiogenic gene of the invention so as to provide the necessary therapeutic effect.

Peptides, phosphopeptides or small organic or inorganic compounds suitable for therapeutic applications may be identified using nucleic acids and polypeptides of the invention in drug screening applications as described below.

Enhancing gene or protein function

Enhancing, stimulating or re-activating a gene's or protein's function can be achieved in a variety of ways. In one aspect of the invention administration of an isolated nucleic acid molecule, as described above, to a subject in need of such treatment may be initiated. Typically, any relevant angiogenic gene of the invention can be administered to a subject to treat or prevent an angiogenesis-related disorder.

In a further aspect, there is provided the use of an isolated nucleic acid molecule, as described above, in the manufacture of a medicament for the treatment of an angiogenesis-related disorder.

Typically, a vector capable of expressing any relevant angiogenic gene, or a fragment or derivative thereof, may be administered to a subject to treat or prevent a disorder including, but not limited to, those described above. Transducing retroviral vectors are often

used for somatic cell gene therapy because of their high efficiency of infection and stable integration and expression. Any relevant full-length gene, or portions thereof, can be cloned into a retroviral vector and expression may be driven from its endogenous promoter or from the retroviral long terminal repeat or from a promoter specific for the target cell type of interest. Other viral vectors can be used and include, as is known in the art, adenoviruses, adeno-associated viruses, vaccinia viruses, papovaviruses, lentiviruses and retroviruses of avian, murine and human origin.

Gene therapy would be carried out according to established methods (Friedman, 1991; Culver, 1996). A vector containing a copy of any relevant angiogenic gene linked to expression control elements and capable of replicating inside the cells is prepared. Alternatively, the vector may be replication deficient and may require helper cells for replication and use in gene therapy.

Gene transfer using non-viral methods of infection *in vitro* can also be used. These methods include direct injection of DNA, uptake of naked DNA in the presence of calcium phosphate, electroporation, protoplast fusion or liposome delivery. Gene transfer can also be achieved by delivery as a part of a human artificial chromosome or receptor-mediated gene transfer. This involves linking the DNA to a targeting molecule that will bind to specific cell-surface receptors to induce endocytosis and transfer of the DNA into mammalian cells. One such technique uses poly-L-lysine to link asialoglycoprotein to DNA. An adenovirus is also added to the complex to disrupt the lysosomes and thus allow the DNA to avoid degradation and move to the nucleus. Infusion of these particles intravenously has resulted in gene transfer into hepatocytes.

Although not identified to date, it is possible that certain individuals with angiogenesis-related disorders contain an abnormality in any one of the angiogenic genes

of the invention. In affected subjects that express a mutated form of any one of the angiogenic genes of the invention it may be possible to prevent the disorder by introducing into the affected cells a wild-type copy of the gene such that it recombines with the mutant gene. This requires a double recombination event for the correction of the gene mutation. Vectors for the introduction of genes in these ways are known in the art, and any suitable vector may be used. Alternatively, introducing another copy of the gene bearing a second mutation in that gene may be employed so as to negate the original gene mutation and block any negative effect.

In a still further aspect, there is provided a method of treating an angiogenesis-related disorder comprising administering a polypeptide, as described above, or an agonist thereof, to a subject in need of such treatment.

In another aspect the invention provides the use of a polypeptide as described above, or an agonist thereof, in the manufacture of a medicament for the treatment of an angiogenesis-related disorder. Examples of such disorders are described above.

In a further aspect, a suitable agonist may also include peptides, phosphopeptides or small organic or inorganic compounds that can mimic the function of any relevant angiogenic gene, or may include an antibody to any relevant angiogenic gene that is able to restore function to a normal level.

Peptides, phosphopeptides or small organic or inorganic compounds suitable for therapeutic applications may be identified using nucleic acids and polypeptides of the invention in drug screening applications as described below.

In further embodiments, any of the agonists, antagonists, complementary sequences, nucleic acid molecules, proteins, antibodies, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the

appropriate agents may be made by those skilled in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, therapeutic efficacy with lower dosages of each agent may be possible, thus reducing the potential for adverse side effects.

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

Modulation of angiogenesis

As the invention has provided a number of genes likely to be involved in angiogenesis it therefore enables methods for the modulation of angiogenesis. In a further aspect of the present invention, any of the methods described above used for the treatment of an angiogenesis-related disorder may be used for the modulation of angiogenesis in any system comprising cells. These systems may include but are not limited to, *in vitro* assay systems (e.g. Matrigel assays, proliferation assays, migration assays, collagen assays, bovine capillary endothelial cell assay etc), *in vivo* assay systems (e.g. *in vivo* Matrigel-type assays, chicken chorioallantoic membrane assay, isolated organs, tissues or cells etc), animal models (e.g. *in vivo* neovascularisation assays, tumour angiogenesis models etc) or hosts in need of treatment (e.g. hosts suffering from angiogenesis-related disorders as previously described.

Drug screening

According to still another aspect of the invention, nucleic acid molecules of the invention as well as peptides of the invention, particularly any relevant purified angiogenic polypeptides or fragments thereof, and

cells expressing these are useful for screening of candidate pharmaceutical compounds in a variety of techniques for the treatment of angiogenesis-related disorders.

Still further, it provides the use wherein high throughput screening techniques are employed.

Compounds that can be screened in accordance with the invention include, but are not limited to peptides (such as soluble peptides), phosphopeptides and small organic or inorganic molecules (such as natural product or synthetic chemical libraries and peptidomimetics).

In one embodiment, a screening assay may include a cell-based assay utilising eukaryotic or prokaryotic host cells that are stably transformed with recombinant nucleic acid molecules expressing the relevant angiogenic polypeptide or fragment, in competitive binding assays. Binding assays will measure for the formation of complexes between the relevant polypeptide or fragments thereof and the compound being tested, or will measure the degree to which a compound being tested will interfere with the formation of a complex between the relevant polypeptide or fragment thereof, and its interactor or ligand.

Non cell-based assays may also be used for identifying compounds that interrupt binding between the polypeptides of the invention and their interactors. Such assays are known in the art and include for example AlphaScreen technology (PerkinElmer Life Sciences, MA, USA). This application relies on the use of beads such that each interaction partner is bound to a separate bead via an antibody. Interaction of each partner will bring the beads into proximity, such that laser excitation initiates a number of chemical reactions ultimately leading to fluorophores emitting a light signal. Candidate compounds that disrupt the binding of the relevant angiogenic polypeptide with its interactor will result in loss of light emission enabling identification and isolation of the responsible compound.

High-throughput drug screening techniques may also employ methods as described in WO84/03564. Small peptide test compounds synthesised on a solid substrate can be assayed through relevant angiogenic polypeptide binding and washing. The relevant bound angiogenic polypeptide is then detected by methods well known in the art. In a variation of this technique, purified angiogenic polypeptides can be coated directly onto plates to identify interacting test compounds.

An additional method for drug screening involves the use of host eukaryotic cell lines that carry mutations in any relevant angiogenic gene of the invention. The host cell lines are also defective at the polypeptide level. Other cell lines may be used where the expression of the relevant angiogenic gene can be regulated (i.e. over-expressed, under-expressed, or switched off). The host cell lines or cells are grown in the presence of various drug compounds and the rate of growth of the host cells is measured to determine if the compound is capable of regulating the growth of defective cells.

The angiogenic polypeptides of the present invention may also be used for screening compounds developed as a result of combinatorial library technology. This provides a way to test a large number of different substances for their ability to modulate activity of a polypeptide. A substance identified as a modulator of polypeptide function may be peptide or non-peptide in nature. Non-peptide "small molecules" are often preferred for many *in vivo* pharmaceutical applications. In addition, a mimic or mimetic of the substance may be designed for pharmaceutical use. The design of mimetics based on a known pharmaceutically active compound ("lead" compound) is a common approach to the development of novel pharmaceuticals. This is often desirable where the original active compound is difficult or expensive to synthesise or where it provides an unsuitable method of administration. In the design of a mimetic, particular

parts of the original active compound that are important in determining the target property are identified. These parts or residues constituting the active region of the compound are known as its pharmacophore. Once found, the pharmacophore structure is modelled according to its physical properties using data from a range of sources including x-ray diffraction data and NMR. A template molecule is then selected onto which chemical groups that mimic the pharmacophore can be added. The selection can be made such that the mimetic is easy to synthesise, is likely to be pharmacologically acceptable, does not degrade *in vivo* and retains the biological activity of the lead compound. Further optimisation or modification can be carried out to select one or more final mimetics useful for *in vivo* or clinical testing.

It is also possible to isolate a target-specific antibody and then solve its crystal structure. In principle, this approach yields a pharmacophore upon which subsequent drug design can be based as described above. It may be possible to avoid protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analogue of the original binding site. The anti-id could then be used to isolate peptides from chemically or biologically produced peptide banks.

Another alternative method for drug screening relies on structure-based rational drug design. Determination of the three dimensional structure of the polypeptides of the invention, or the three dimensional structure of the protein complexes which may incorporate these polypeptides allows for structure-based drug design to identify biologically active lead compounds.

Three dimensional structural models can be generated by a number of applications, some of which include experimental models such as x-ray crystallography and NMR

and/or from *in silico* studies using information from structural databases such as the Protein Databank (PDB). In addition, three dimensional structural models can be determined using a number of known protein structure prediction techniques based on the primary sequences of the polypeptides (e.g. SYBYL - Tripos Associated, St. Louis, MO), *de novo* protein structure design programs (e.g. MODELER - MSI Inc., San Diego, CA, or MOE - Chemical Computing Group, Montreal, Canada) or *ab initio* methods (e.g. see US Patent Numbers 5331573 and 5579250).

Once the three dimensional structure of a polypeptide or polypeptide complex has been determined, structure-based drug discovery techniques can be employed to design biologically active compounds based on these three dimensional structures. Such techniques are known in the art and include examples such as DOCK (University of California, San Francisco) or AUTODOCK (Scripps Research Institute, La Jolla, California). A computational docking protocol will identify the active site or sites that are deemed important for protein activity based on a predicted protein model. Molecular databases, such as the Available Chemicals Directory (ACD) are then screened for molecules that complement the protein model.

Using methods such as these, potential clinical drug candidates can be identified and computationally ranked in order to reduce the time and expense associated with typical 'wet lab' drug screening methodologies.

Compounds identified from the screening methods described above form a part of the present invention, as do pharmaceutical compositions containing these and a pharmaceutically acceptable carrier.

Pharmaceutical Preparations

Compounds identified from screening assays as indicated above can be administered to a patient at a therapeutically effective dose to treat or ameliorate a disorder associated with angiogenesis. A therapeutically

effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of the disorder.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals. The data obtained from these studies can then be used in the formulation of a range of dosages for use in humans.

Pharmaceutical compositions for use in accordance with the present invention can be formulated in a conventional manner using one or more physiological acceptable carriers, excipients or stabilisers which are well known. Acceptable carriers, excipients or stabilizers are non-toxic at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including absorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; binding agents including hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or non-ionic surfactants such as Tween, Pluronics or polyethylene glycol (PEG).

The formulation of pharmaceutical compositions for use in accordance with the present invention will be based on the proposed route of administration. Routes of administration may include, but are not limited to, inhalation, insufflation (either through the mouth or nose), oral, buccal, rectal or parental administration.

Diagnostic and prognostic applications

Should abnormalities in any one of the angiogenic genes of the invention exist, which alter activity and/or

expression of the gene to give rise to angiogenesis-related disorders, the polynucleotides and polypeptides of the invention may be used for the diagnosis or prognosis of these disorders, or a predisposition to such disorders. Examples of such disorders include, but are not limited to, cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis, cardiovascular diseases such as atherosclerosis, ischaemic limb disease and coronary artery disease. Diagnosis or prognosis may be used to determine the severity, type or stage of the disease state in order to initiate an appropriate therapeutic intervention.

In another embodiment of the invention, the polynucleotides that may be used for diagnostic or prognostic purposes include oligonucleotide sequences, genomic DNA and complementary RNA and DNA molecules. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which abnormal expression or mutations in any one of the angiogenic genes may be correlated with disease. Genomic DNA used for the diagnosis or prognosis may be obtained from body cells, such as those present in the blood, tissue biopsy, surgical specimen, or autopsy material. The DNA may be isolated and used directly for detection of a specific sequence or may be amplified by the polymerase chain reaction (PCR) prior to analysis. Similarly, RNA or cDNA may also be used, with or without PCR amplification. To detect a specific nucleic acid sequence, direct nucleotide sequencing, reverse transcriptase PCR (RT-PCR), hybridization using specific oligonucleotides, restriction enzyme digest and mapping, PCR mapping, RNAse protection, and various other methods may be employed. Oligonucleotides specific to particular sequences can be chemically synthesized and labelled radioactively or nonradioactively and hybridized to individual samples immobilized on membranes or other solid-supports or in solution. The presence, absence or excess expression of

any one of the angiogenic genes may then be visualized using methods such as autoradiography, fluorometry, or colorimetry.

In a particular aspect, the nucleotide sequences of the invention may be useful in assays that detect the presence of associated disorders, particularly those mentioned previously. The nucleotide sequences may be labelled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis or prognosis of an angiogenesis-related disorder associated with a mutation in any one of the angiogenic genes of the invention, the nucleotide sequence of the relevant gene can be compared between normal tissue and diseased tissue in order to establish whether the patient expresses a mutant gene.

In order to provide a basis for the diagnosis or prognosis of a disorder associated with abnormal expression of any one of the angiogenic genes of the invention, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding the relevant angiogenic gene, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values

obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Another method to identify a normal or standard profile for expression of any one of the angiogenic genes is through quantitative RT-PCR studies. RNA isolated from body cells of a normal individual, particularly RNA isolated from endothelial cells, is reverse transcribed and real-time PCR using oligonucleotides specific for the relevant gene is conducted to establish a normal level of expression of the gene. Standard values obtained in both these examples may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays or quantitative RT-PCR studies may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

According to a further aspect of the invention there is provided the use of an angiogenic polypeptide as described above in the diagnosis or prognosis of an angiogenesis-related disorder associated with any one of angiogenic genes of the invention, or a predisposition to such disorders.

When a diagnostic or prognostic assay is to be based upon any relevant angiogenic polypeptide, a variety of approaches are possible. For example, diagnosis or prognosis can be achieved by monitoring differences in the electrophoretic mobility of normal and mutant proteins. Such an approach will be particularly useful in identifying mutants in which charge substitutions are present, or in which insertions, deletions or

substitutions have resulted in a significant change in the electrophoretic migration of the resultant protein. Alternatively, diagnosis or prognosis may be based upon differences in the proteolytic cleavage patterns of normal and mutant proteins, differences in molar ratios of the various amino acid residues, or by functional assays demonstrating altered function of the gene products.

In another aspect, antibodies that specifically bind the relevant angiogenic gene product may be used for the diagnosis or prognosis of disorders characterized by abnormal expression of the gene, or in assays to monitor patients being treated with the relevant angiogenic gene or protein or agonists, antagonists, or inhibitors thereof. Antibodies useful for diagnostic or prognostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic or prognostic assays may include methods that utilize the antibody and a label to detect the relevant protein in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labelled by covalent or non-covalent attachment of a reporter molecule.

A variety of assays for measuring the relevant angiogenic polypeptide based on the use of antibodies specific for the polypeptide are known in the art and provide a basis for diagnosing altered or abnormal levels of expression. Normal or standard values for expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to the relevant protein under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods which are known in the art. Examples include, but are not limited to, enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), immunofluorescence, flow cytometry, histology, electron microscopy, in situ assays, immunoprecipitation, Western blot etc. For example, using

the ELISA technique an enzyme which is bound to the antibody will react with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety that can be detected for example by spectrophotomeric, fluorimetric or by visual means. Detection may also be accomplished by using other assays such as RIAs where the antibodies or antibody fragments are radioactively labelled. It is also possible to label the antibody with a fluorescent compound. When the fluorescently labelled antibody is exposed to light of a certain wavelength, its presence can then be detected due to fluorescence. The antibody can also be detectably labelled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction.

Quantities of protein expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing or prognosing disease.

Once an individual has been diagnosed or prognosed with a disorder, effective treatments can be initiated, as described above. In the treatment of angiogenesis-related diseases which are characterised by uncontrolled or enhanced angiogenesis, the expanding vasculature needs to be inhibited. This would involve inhibiting the relevant angiogenic genes or proteins of the invention that promote angiogenesis. In addition, treatment may also need to stimulate expression or function of the relevant angiogenic genes or proteins of the invention whose normal role is to inhibit angiogenesis but whose activity is reduced or absent in the affected individual.

In the treatment of angiogenesis-related diseases which are characterised by inhibited or decreased angiogenesis, approaches which enhance or promote vascular expansion are desirable. This may be achieved using

methods essentially as described above but will involve stimulating the expression or function of the relevant angiogenic gene or protein whose normal role is to promote angiogenesis but whose activity is reduced or absent in the affected individual. Alternatively, inhibiting genes or proteins that restrict angiogenesis may also be an approach to treatment.

Microarray

In further embodiments, complete cDNAs, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as probes in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of angiogenesis-related disorders, to diagnose or prognose angiogenesis-related disorders, and to develop and monitor the activities of therapeutic agents. Microarrays may be prepared, used, and analysed using methods known in the art. (For example, see Schena et al., 1996; Heller et al., 1997).

Transformed hosts

The present invention also provides for the production of genetically modified (knock-out, knock-in and transgenic), non-human animal models comprising the nucleic acid molecules of the invention. These animals are useful for the study of the function of the relevant angiogenic gene, to study the process of angiogenesis, to study the mechanisms of angiogenic disease as related to these genes, for the screening of candidate pharmaceutical compounds for the treatment of angiogenesis-related disorders, for the creation of explanted mammalian cell cultures which express the protein or mutant protein, and for the evaluation of potential therapeutic interventions.

Animal species which are suitable for use in the animal models of the present invention include, but are not limited to, rats, mice, hamsters, guinea pigs, rabbits, dogs, cats, goats, sheep, pigs, and non-human primates such as monkeys and chimpanzees. For initial studies, genetically modified mice and rats are highly desirable due to the relative ease in generating knock-in, knock-out or transgenics of these animals, their ease of maintenance and their shorter life spans. For certain studies, transgenic yeast or invertebrates may be suitable and preferred because they allow for rapid screening and provide for much easier handling. For longer term studies, non-human primates may be desired due to their similarity with humans.

To create an animal model based on any one of the angiogenic genes of the invention, several methods can be employed. These include, but are not limited to, generation of a specific mutation in a homologous animal gene, insertion of a wild type human gene and/or a humanized animal gene by homologous recombination, insertion of a mutant (single or multiple) human gene as genomic or minigene cDNA constructs using wild type, mutant or artificial promoter elements, or insertion of artificially modified fragments of the endogenous gene by homologous recombination. The modifications include insertion of mutant stop codons, the deletion of DNA sequences, or the inclusion of recombination elements (lox p sites) recognized by enzymes such as Cre recombinase.

To create transgenic mice in order to study gain of gene function *in vivo*, any relevant angiogenic gene can be inserted into a mouse germ line using standard techniques such as oocyte microinjection. Gain of gene function can mean the overexpression of a gene and its protein product, or the genetic complementation of a mutation of the gene under investigation. For oocyte injection, one or more copies of the wild type or mutant gene can be inserted into the pronucleus of a just-fertilized mouse oocyte.

This oocyte is then reimplanted into a pseudo-pregnant foster mother. The liveborn mice can then be screened for integrants using analysis of tail DNA for the presence of the relevant human angiogenic gene sequence. The transgene can be either a complete genomic sequence injected as a YAC, BAC, PAC or other chromosome DNA fragment, a cDNA with either the natural promoter or a heterologous promoter, or a minigene containing all of the coding region and other elements found to be necessary for optimum expression.

To generate knock-out mice or knock-in mice, gene targeting through homologous recombination in mouse embryonic stem (ES) cells may be applied. Knock-out mice are generated to study loss of gene function *in vivo* while knock-in mice allow the study of gain of function or to study the effect of specific gene mutations. Knock-in mice are similar to transgenic mice however the integration site and copy number are defined in the former.

For knock-out mouse generation, gene targeting vectors can be designed such that they disrupt (knock-out) the protein coding sequence of the relevant angiogenic gene in the mouse genome. Knock-out animals of the invention will comprise a functional disruption of a relevant angiogenesis gene of the invention such that the gene does not express a biologically active product. It can be substantially deficient in at least one functional activity coded for by the gene. Expression of the polypeptide encoded by the gene can be substantially absent (i.e. essentially undetectable amounts are made) or may be deficient in activity such as where only a portion of the gene product is produced. In contrast, knock-in mice can be produced whereby a gene targeting vector containing the relevant angiogenic gene can integrate into a defined genetic locus in the mouse genome. For both applications, homologous recombination is catalysed by specific DNA repair enzymes that recognise homologous DNA sequences and exchange them via double crossover.

Gene targeting vectors are usually introduced into ES cells using electroporation. ES cell integrants are then isolated via an antibiotic resistance gene present on the targeting vector and are subsequently genotyped to identify those ES cell clones in which the gene under investigation has integrated into the locus of interest. The appropriate ES cells are then transmitted through the germline to produce a novel mouse strain.

In instances where gene ablation results in early embryonic lethality, conditional gene targeting may be employed. This allows genes to be deleted in a temporally and spatially controlled fashion. As above, appropriate ES cells are transmitted through the germline to produce a novel mouse strain, however the actual deletion of the gene is performed in the adult mouse in a tissue specific or time controlled manner. Conditional gene targeting is most commonly achieved by use of the cre/lox system. The enzyme cre is able to recognise the 34 base pair loxP sequence such that loxP flanked (or floxed) DNA is recognised and excised by cre. Tissue specific cre expression in transgenic mice enables the generation of tissue specific knock-out mice by mating gene targeted floxed mice with cre transgenic mice. Knock-out can be conducted in every tissue (Schwenk et al., 1995) using the 'deleter' mouse or using transgenic mice with an inducible cre gene (such as those with tetracycline inducible cre genes), or knock-out can be tissue specific for example through the use of the CD19-cre mouse (Rickert et al., 1997).

According to still another aspect of the invention there is provided the use of genetically modified non-human animals for the screening of candidate pharmaceutical compounds.

It will be clearly understood that, although a number of prior art publications are referred to herein, this reference does not constitute an admission that any of these documents forms part of the common general knowledge

in the art, in Australia or in any other country. Throughout this specification and the claims, the words "comprise", "comprises" and "comprising" are used in a non-exclusive sense, except where the context requires otherwise.

Brief Description of the Drawings

Figure 1. Example of the expression profile of selected differentially expressed clones during defined time points in the *in vitro* model of angiogenesis. Time points at the defined stages of 0.5 hours, 3 hours, 6 hours and 24 hours of the *in vitro* tube formation assay were plotted against the log ratio of cy5 (red) and cy3 (green) dyes used for microarray hybridizations. A: example of a clone with peak expression at the 0.5 hour time point; B: example of a clone with peak expression at the 3 hour time point; C: example of a clone with peak expression at the 6 hour time point; and D: example of a clone with peak expression at the 24 hour time point.

Figure 2. Expression profile of differentially expressed genes BNO782 and BNO481. Both genes show peak expression at the 6 hour time point of the *in vitro* tube formation assay. A: BNO782; B: BNO481.

Figure 3. Analysis of the level of BNO782 expression knock-down mediated by BNO782 siRNA2 and BNO481 expression knock-down mediated by BNO481 siRNA1, as measured by real-time RT-PCR. The three siRNA oligonucleotides targeted to each gene were able to reduce expression of the gene to varying degrees with BNO781 siRNA2 inhibiting BNO781 expression by 24% (A) and BNO481 siRNA1 inhibiting expression of BNO481 by 36% (B).

Figure 4. Reducing BNO782 or BNO481 mRNA expression inhibits HUVEC tube formation. HUVECs infected with BNO782 siRNA2, BNO481 siRNA1, or a vector control were plated on Matrigel for 24hrs. Vector infected cells formed extensive networks of tube structures (A and C). In contrast, cells infected with BNO782 siRNA2 or BNO481 siRNA1 exhibited

tube structure networks of significantly reduced complexity with a high number of incomplete tube extensions (B and D).

Modes for Performing the Invention

Example 1: *In vitro* capillary tube formation

The *in vitro* model of angiogenesis is essentially as described in Gamble et al (1993). The assay was performed in collagen under the stimulation of phorbol myristate acetate (PMA) and the anti-integrin ($\alpha_2\beta_1$) antibody, RMACII. Human umbilical vein endothelial cells (HUVECs) were used in all experiments between passages 2 to 4.

Cells were harvested from bulk cultures (t=0), replated onto the collagen gels with stimulation and then harvested from the collagen gels at 0.5, 3.0, 6.0 and 24 hours after commencement of the assay. These time points were chosen since major morphological changes occur at these stages. Briefly, by 0.5 hours, cells have attached to the collagen matrix and have commenced migration into the gel. By 3.0 hours, small intracellular vesicles are visible. By 6.0 hours, these vesicles are coalescing together to form membrane bound vacuoles and the cells in the form of short sprouts have invaded the gel. After this time, these vacuoles fuse with the plasma membrane, thus expanding the intercellular space to generate the lumen (Meyer et al., 1997). The formation of these larger vacuoles is an essential requirement of lumen formation (Gamble et al., 1999). By 24 hours, the overall anastomosing network of capillary tubes has formed and has commenced degeneration.

Example 2: RNA isolation, cDNA synthesis and amplification

Cells harvested at the specified time points were used for the isolation of total RNA using the Trizol reagent (Gibco BRL) according to manufacturers conditions. SMART (Switching mechanism at 5' end of RNA transcript) technology was used to convert small amounts of total RNA

into enough cDNA to enable cDNA subtraction to be performed (see below). This was achieved using the SMART-PCR cDNA synthesis kit (Clontech-user manual PT3041-1) according to manufacturers recommendations. The SMART-PCR cDNA synthesis protocol generated a majority of full length cDNAs which were subsequently PCR amplified for cDNA subtraction.

Example 3: Suppression subtractive hybridization (SSH)

SSH was performed on SMART amplified cDNA in order to enrich for cDNAs that were either up-regulated or down-regulated between the cDNA populations defined by the selected time-points. This technique also allowed "normalisation" of the regulated cDNAs, thereby making low abundance cDNAs (i.e. poorly expressed, but important, genes) more easily detectable. To do this, the PCR-Select cDNA synthesis kit (Clontech-user manual PT3041-1) and PCR-Select cDNA subtraction kit (Clontech-user manual PT1117-1) were used based on manufacturers conditions. These procedures relied on subtractive hybridization and suppression PCR amplification. SSH was performed between the following populations: 0 - 0.5 hours; 0.5 - 3.0 hours; 3.0 - 6.0 hours; 6.0 - 24 hours.

Example 4: Differential screening of cDNA clones

Following SSH, the cDNA fragments were digested with *Eag*I and cloned into the compatible unique *Not*I site in pBluescript KS$^+$ using standard techniques (Sambrook et al., 1989). This generated forward and reverse subtracted libraries for each time period. Initially, the forward subtracted libraries were used in subsequent studies to identify those clones representing genes that were up-regulated in their expression during the *in vitro* model of angiogenesis. To do this, a microarray analysis procedure was adopted.

Microarray slide preparation

A total of 10,000 clones from the 4 forward subtracted libraries (3,200 clones from 0-0.5 hr; 3,000 clones from 0.5-3 hr; 2,800 clones from 3-6 hr; 1,000 clones from 6-24 hr) were chosen to construct microarray slides. Inserts from these clones were amplified using standard PCR techniques with flanking T3 and T7 pBluescript KS^+ vector primers. DNA from each clone was spotted in duplicate onto a single microarray slide. Appropriate positive and negative controls were also incorporated onto the plate.

Probe labelling

Human umbilical vein endothelial cells harvested at the specified time points (0, 0.5, 3, 6, and 24 hr) were used for the isolation of total RNA using the Trizol reagent (Gibco BRL) according to manufacturers conditions. From each time point, 0.5 ug of total RNA was used as a template for the amplification of antisense RNA (aRNA) using the Ambion MessageAmp™ aRNA Kit. Briefly, total RNA was reversed transcribed with a T7 oligo(dT) primer in order to synthesize cDNA containing a T7 promoter sequence extending from the poly(A) tails of messages generated by reverse transcription. The cDNA was converted to a double-stranded DNA template and used for *in vitro* transcription of aRNA, incorporating 5-(3-aminoallyl)-UTP so as to allow coupling of fluorescent CyDyes. A typical amplification reaction would yield approximately 10 ug of mRNA (>400X amplification, assuming the initial total RNA contained <5% mRNA).

Microarray hybridization

After coupling of CyDyes, the synthesized aRNA was used as a probe (3.0-3.5 ug) for hybridization to a microarray slide. The hybrizations performed were as follows:

1. 0 vs 0.5h (6 slides, 3 Dye swaps)
2. 0 vs 3h (4 slides, 2 Dye swaps)
3. 0 vs 6h (4 slides, 2 Dye swaps)
4. 0 vs 24h (4 slides, 2 Dye swaps)

Multiple slides were hybridized for each time point in order to verify the result from any one hybridization. Slides were hybridized in chambers for 16 hours, washed, and then scanned using the GenePix 2000 scanner. Those clones that were shown to be highly up-regulated were chosen for further analysis.

In summary, SSH was used in combination with microarray analyses to identify genes that are up-regulated and may be involved in biological processes underlying endothelial cell activation and blood vessel formation. This approach is novel in that it involves nucleotide hybridization steps that aim to reduce gene detection redundancy and enhance the chances of detecting genes that are of low overall representation in the endothelial cell transcriptome. The nucleotide-based sequential time-points aims to detect the timepoint at which the up-regulation of a particular gene takes place in a way that reduces redundancy of detection. For example, a gene that is up-regulated at 3hrs, and its expression remains up-regulated in subsequent time-points, will only be detected in the 0.5-3hr subtraction step. In contrast, if subtractions were done with the 0hr timepoint for all subsequent timepoints then this example gene would be detected at all subtraction steps following the 3hrs timepoint subtraction. This would introduce redundancy that could result in masking the possible detection of other genes of lower representation in the endothelial cell mRNA expression pool. The subsequent use of microarray analysis is based on the comparison subtraction hybridization in the SSH step involving each timepoint with the 0hrs timepoint. This enables the expression profiling of each gene across all timepoints in relation

to 0hrs, irrespective of the timepoint at which it is up-regulated.

Example 5: Clone selection

From analysis of the microarray hybridizations, a total of 1,963 clones were identified to be up-regulated in their expression at specified time points during the *in vitro* model of angiogenesis. Figure 1 provides an example of the expression profiles observed during defined time points in the *in vitro* model for a selection of clones. Each of the 1,963 clones were sequenced and subsequent *in silico* database analysis was used to remove clones containing vector sequences only and clones for which poor sequence was obtained. Following this, redundancy screens were used to group clones according to individual genes that they represented. This left a total of 523 genes that were found to be up-regulated in their expression during the process of angiogenesis.

Tables 1, 2 and 3 provide information on the up-regulated clones that were sequenced. Table 1 includes those clones which represent previously uncharacterised or novel genes, while Table 2 includes clones that correspond to previously identified genes which have not before been associated with angiogenesis. Also identified were a number of genes that have previously been shown to be involved in the process of angiogenesis (Table 3). The identification of these clones provides a validation or proof of principle of the effectiveness of the angiogenic gene identification strategy employed and suggests that the clones listed in Tables 1 and 2 are additional angiogenic gene candidates.

Example 6: Analysis of the angiogenic genes

Further evidence for the involvement of the genes in Tables 1 and 2 in angiogenesis can be obtained through the functional analysis of each gene, for example by examining the effect that knock-down of their expression has on

endothelial cell (EC) function and capillary tube formation.

A number of knock-down technologies and assays may be used. For example full-length coding sequences of the genes can be cloned into suitable expression vectors such as retroviruses or adenoviruses in both sense and anti-sense orientations and used for infection into ECs. Retrovirus infection gives long-term EC lines expressing the gene of interest whereas adenovirus infection gives transient gene expression. Infected cells can then be subjected to a number of EC assays including proliferation and capillary tube formation to confirm the role of each gene in angiogenesis.

In this study RNA interference (RNAi) gene knock-down technology was used for the analysis of gene function (see detailed description below). In this technique, short gene-specific RNA oligonucleotides are delivered to ECs in culture mediated by retroviral infection. These oligonucleotides bind to the gene transcript under study and induce its degradation resulting in silencing or reduction of gene expression. The consequences of this alteration to gene expression can be subsequently studied using assays that examine the ability of ECs to proliferate, migrate and form capillaries in vitro. The RNAi procedure adopted in this study is described below in detail and documents the analysis of two of the identified up-regulated angiogenesis genes. One of these genes is BNO782 shown in Table 1, a novel gene whose expression peaks at the 6 hour time point of the *in vitro* angiogenesis model (Figure 2A), while the other gene is BNO481 (KPNA4) as shown in Table 2, which is a previously identified gene that has not before been shown to have a role in angiogenesis. The expression of BNO481 also peaks at the 6 hour time point of the *in vitro* angiogenesis model (Figure 2B).

RNAi oligonucleotide design

Short interfering RNA (siRNA) oligonucleotides for RNAi-mediated knock-down of BNO782 and BNO481 were identified through application of in-house computer software. This software incorporates a series of parameters for selecting appropriate siRNA oligonucleotides. These parameters ensure that the siRNA sequence starts after an AA dinucleotide, the siRNA is in the open reading frame of the gene and 100 bp downstream the ATG start codon, the GC content of the siRNA is between 35% and 60%, and the siRNA does not have stretches of more than three T, A, C or G nucleotides. siRNA sequences that harbour low complexity regions were not used. In addition, BLAST analysis was used to select against probes that cross-hybridize with a number of genes (Blastn_refseq at "expect 500" and "word size 7" and alignment scores accepted at 19>score>15 where: alignment score = length_match - (gap+mismatch). siRNAs were synthesised in hair-pin format for cloning into retroviral vectors. For each gene, three siRNA oligonucleotides were selected with each one being examined individually for their effects on gene-knock-down and EC function.

Retroviral infection of HUVE cells

Each siRNA oligonucleotide was cloned into a retroviral vector for the delivery of the oligonucleotide to human umbilical vein endothelial cells (HUVECs). The siRNA vector was constructed through a modification of pMSCVpuro (BD Biosciences). Briefly, the 3'LTR of pMSCVpuro was inactivated by removal of the XbaI/NheI fragment. A H1-RNA Polymerase III promoter cassette was then inserted into the MCS of the vector. Annealed siRNA primers were ligated into the modified vector (pMSCVpuro(H1)) digested with BglII and HindIII restriction enzymes.

For virus production prior to infection of HUVECs, 293T cells were plated at a density of 1 x 10^6 cells per

well of a 6 well plate 18-24 hours before transfection in RPMI media (Invitrogen) supplemented with 10% FCS (Invitrogen) and 1.0 M Hepes (Invitrogen) without antibiotics. Cells were co-transfected with 2 µg retroviral DNA and 1.5 µg pVPack-VSV-G (Stratagene), 1.5 µg pVPack-GP (Stratagene) using Lipofectamine 2000 reagent (Invitrogen). Transfected cells were incubated overnight in 5% CO_2 at 37°C. The following day, media containing the DNA/LF2000 complexes was removed and replaced with RPMI supplemented with 10% FCS, 1.0 M Hepes and 1% PSG (Invitrogen). Virus containing supernatants were collected 48-72 hours post transfection and filtered using a 0.45 µM filter. Virus was aliquoted and stored at -80°C.

For the retroviral infection of HUVECs (Clonetics), cells were plated 24 hours before infection in EGM-2 media (Clonetics) at a density of 1.3 x 10^5 cells per well of a 6 well plate. The following day, 500 µl of virus supernatant was combined with 500 µl of EGM-2 complete media. Polybrene (Sigma) was added to a final concentration of 8.0 µg/ml. Media was aspirated from the cells and replaced with the viral mix. Cells were incubated with the viral mix in 5% CO_2 at 37°C. After 3 hours incubation, an additional 1.0 ml of EGM-2 media was added and cells were incubated for a further 24 hours. After this time HUVE cells were split 1:2 and replated into a 6 well plate. Cells were incubated for 24 hours following splitting to allow them to recover and adhere. To select for infected cells, medium was replaced with EGM-2 complete medium containing puromycin (Sigma) at a 0.4 µg/ml final concentration. Cells were incubated until uninfected cells treated with puromycin had died and infected resistant cells had grown to confluence. Media containing puromycin was replaced every 48 hours to replenish puromycin and remove cell debris. Once resistant cells were grown to confluence (approximately 4-5 days after starting selection), cells were washed in PBS, trypsinised and

their properties analysed using the Matrigel capillary tube formation assay.

Capillary tube formation assay

96 well tissue culture plates were coated with 50 µl of cold Matrigel (BD Biosciences) at 4°C in a two layer process. Matrigel was allowed to polymerize at 37°C for a minimum of 30 minutes before being used. Trypsinised cells were collected in 500 µl of EGM-2 media then centrifuged at 400 rcf for 3 minutes to pellet cells. This allows for the removal of trypsin that may interfere with the assay. Cell pellets were resuspended in 500 µl EGM-2 media then counted using a heamocytometer. Cells were diluted to 2.5 x 10^5 cells/ml in EGM-2 media. 100µl of the diluted cell suspension was added to duplicate Matrigel coated wells. The final cell density was 25,000 cells/well. Plates were incubated for 22 hours in a humidified incubator at 37°C with 5% CO_2. Images were obtained using an Olympus BX-51 microscope with a 4x objective and Optronics MagnaFire software. Remaining cells were pelleted at 400 rcf for 3 minutes, then media was removed and pellets stored at -80°C for extraction of RNA for real-time RT-PCR analysis (see below). For all assays performed, a vector control was included. This consisted of HUVECs undergoing the infection and selection process with virus made for the vector containing no siRNA insert. This allows for comparison of capillary tube formation ability between a control (vector) and the individual siRNA under analysis.

Real-time RT-PCR analysis

To determine the level of gene knock-down (mediated by the siRNAs) occurring in the HUVECs, real-time RT-PCR was employed. This involved isolation of RNA from infected cells using the RNeasy Mini or Midi kits (Qiagen) as per manufacturer's instructions (including the on-column DNase treatment). Total RNA was visualised on a 1.2% TBE agarose gel containing ethidium bromide to check for quality and

purity. Total RNA concentration was determined by A_{260} on a spectrophotometer.

For the synthesis of cDNA, total RNA (at least 1ug and preferably at a concentration >1.0 ug/ul) was reverse transcribed using M-MLV (Promega) as per manufacturer's directions. Briefly, the RNA sample to be analysed was made up to 13 ul with water and 1.0 ul of oligo-dT primer (500ng/ul) was added. After incubating at 70°C for 5 minutes, the tubes were placed on ice for 5 minutes and 11 ul of a pre-made master mix containing 5.0 ul M-MLV RT 5x Reaction Buffer, 1.25 ul 10 mM dNTP mix, 1.0 ul of M-MLV RT (H^- point mutant) enzyme, and 3.75 ul water was added. This mix was incubated at 40°C for one hour, and the reaction terminated by incubating at 70°C for 15 minutes.

Real-Time PCRs were run on the RotorGene™ 2000 system (Corbett Research). Reactions used AmpliTaq Gold enzyme (Applied Biosystems) and followed the manufacturers instructions. Real-Time PCR reactions were typically performed in a volume of 25 ul and consisted of 1X AmpliTaq Gold Buffer, 200 nM dNTP mix, 2.0 mM $MgCl_2$ (may vary for primer combination used), 0.3 uM of each primer, 1X SYBR Green mix (Cambrex BioScience Rockland Inc), 1.2 ul of AmpliTaq Gold Enzyme, and 10 ul of a 1 in 5 dilution of the cDNA template.

Cycling conditions were typically performed at 94°C for 12 minutes, followed by 35 cycles of 94°C for 15 seconds, 60°C for 15 seconds, and 72°C for 20 seconds. The annealing temperature of the primers may vary depending on the properties of the primers used.

The PCR cycling was followed by the generation of a melt curve using the RotorGene™ 2000 software where the amount of annealed product was determined by holding at each degree between 50°C and 99°C and measuring the absorbance. All products were run on a 1.2% agarose gel containing ethidium bromide to check specificity in addition to observing the melt curve.

The level of knock-down of a particular gene was then

measured by a comparison of its expression level in HUVECs infected with the relevant siRNA under investigation as opposed to HUVECs infected with the retroviral vector alone.

In vitro regulation of HUVEC function - BNO782 and BNO481

The siRNA oligonucleotides designed to knock-down BNO782 and BNO481 expression are represented by SEQ ID Numbers: 45-47 and SEQ ID Numbers: 48-50 respectively. Real-time RT-PCR analysis of HUVECs retrovirally infected with these siRNAs revealed that each siRNA was able to knock-down the expression of BNO782 or BNO481 to varying degrees. The level of BNO782 expression knock-down mediated by BNO782 siRNA2 (SEQ ID NO: 46) was 24% (Figure 3A), while expression of BNO481 was reduced by 36% (Figure 3B) using BNO481 siRNA1 (SEQ ID NO: 48). Both of these siRNAs were subsequently used separately in Matrigel assays to examine the effects that this level of knock-down for each gene had on the ability of HUVECs to participate in capillary tube formation. As can be seen in Figure 4, reducing BNO782 or BNO481 mRNA levels inhibits HUVEC tube formation. Vector infected cells formed extensive networks of tube structures (Figure 4A and 4C) while cells infected with BNO782 siRNA2 or BNO481 siRNA1 exhibited tube structure networks of significantly reduced complexity with a high number of incomplete tube extensions (Figure 4B and 4D). This result confirms a role for both BNO782 and BNO481 in the process of angiogenesis.

Protein interaction studies

The ability of any one of the angiogenic proteins of the invention, including BNO782 and BNO481, to bind known and unknown proteins can be examined. Procedures such as the yeast two-hybrid system are used to discover and identify any functional partners. The principle behind the yeast two-hybrid procedure is that many eukaryotic transcriptional activators, including those in yeast,

consist of two discrete modular domains. The first is a DNA-binding domain that binds to a specific promoter sequence and the second is an activation domain that directs the RNA polymerase II complex to transcribe the gene downstream of the DNA binding site. Both domains are required for transcriptional activation as neither domain can activate transcription on its own. In the yeast two-hybrid procedure, the gene of interest or parts thereof (BAIT), is cloned in such a way that it is expressed as a fusion to a peptide that has a DNA binding domain. A second gene, or number of genes, such as those from a cDNA library (TARGET), is cloned so that it is expressed as a fusion to an activation domain. Interaction of the protein of interest with its binding partner brings the DNA-binding peptide together with the activation domain and initiates transcription of the reporter genes. The first reporter gene will select for yeast cells that contain interacting proteins (this reporter is usually a nutritional gene required for growth on selective media). The second reporter is used for confirmation and while being expressed in response to interacting proteins it is usually not required for growth.

The nature of the interacting genes and proteins can also be studied such that these partners can also be targets for drug discovery.

Structural studies

Recombinant angiogenic proteins of the invention can be produced in bacterial, yeast, insect and/or mammalian cells and used in crystallographical and NMR studies. Together with molecular modeling of the protein, structure-driven drug design can be facilitated.

TABLE 1

Novel Angiogenesis Genes

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO605	BNO605	EST, UI-HF-BR0p-ajy-c-08-0-UI.s1 Homo sapiens cDNA	None	AW576601	
BNO612	FLJ20445	hypothetical protein FLJ20445	Hs.343748	NM_017824	6
BNO616	MGC2747	hypothetical protein MGC2747	Hs.194017	NM_024104	0.5, 6
BNO617	FLJ20986	hypothetical protein FLJ20986	Hs.324507	NM_024524	6
BNO618	FLJ14834	hypothetical protein FLJ14834	Hs.62905	NM_032849	3
BNO620	FLJ22746	hypothetical protein FLJ22746	Hs.147585	NM_024785	0.5
BNO622	KIAA1376	KIAA1376 protein	Hs.24684	BC015928	3, 24
BNO627	BNO627	EST, AV756199 BM Homo sapiens cDNA clone BMFAUH02 5'	None	SEQ ID NO: 1	6
BNO628	BNO628	EST, QV1-BT0631-130300-111-e03 BT0631 Homo sapiens cDNA	None	SEQ ID NO: 2	6
BNO629	BNO629	EST, Homo sapiens cDNA clone IMAGE:2664022 3'	None	SEQ ID NO: 3	6
BNO630	BNO630	EST, Homo sapiens cDNA clone IMAGE:2357465 3'	None	SEQ ID NO: 4, 51	6
BNO632	BNO632	ESTs	Hs.404198	SEQ ID NO: 5	6
BNO633	BNO633	ESTs, Weakly similar to hypothetical protein FLJ20378	Hs.310598	SEQ ID NO: 6	24
BNO634	BNO634	ESTs	Hs.345443	SEQ ID NO: 7	6
BNO635	BNO635	Hypothetical protein	Hs.54347	BC057847	6
BNO636	BNO636	ESTs	Hs.105636	SEQ ID NO: 8	3
BNO637	BNO637	ESTs	Hs.486928	SEQ ID NO: 9, 52	6
BNO638	BNO638	EST	None	SEQ ID NO: 10	6
BNO639	BNO639	None	None	SEQ ID NO: 11, 53	6
BNO640	BNO640	None	None	SEQ ID NO: 12	6
BNO645	FLJ10498	hypothetical protein FLJ10498	Hs.270107	NM_018115	24
BNO648	LOC57146	hypothetical protein from clone 24796	Hs.27191	NM_020422	0.5
BNO652	FLJ31051	hypothetical protein FLJ31051	Hs.406199	NM_153687	6
BNO655	LOC51122	HSPC042 protein	Hs.432729	NM_016094	3
BNO659	FLJ32123	FLJ32123	Hs.349397	AK056685	6
BNO662	BNO662	ESTs	Hs.444495	BX647355	6
BNO664	FLJ10312	FLJ10312	None	NM_030672	3
BNO669	BNO669	ESTs	Hs.172998	BC030094	3

TABLE 1 (Continued)

Novel Angiogenesis Genes

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO671	KIAA0882	KIAA0882 protein	Hs.411317	AB020689	3
BNO673	BNO673	hypothetical protein DKFZp434L142	Hs.323583	NM_016613	6
BNO675	FLJ10700	hypothetical protein FLJ10700	Hs.295909	NM_018182	3
BNO677	FLJ30135	FLJ30135	Hs.34906	BC020494	3, 24
BNO685	FLJ10849	hypothetical protein FLJ10849	Hs.386784	NM_018243	
BNO687	MGC45416	hypothetical protein MGC45416	Hs.95835	NM_152398	24
BNO690	C15orf15	chromosome 15 open reading frame 15	Hs.274772	NM_016304	3
BNO694	BNO694	cDNA DKFZp566E0124	None	AL050030	6
BNO697	BNO697	Hypothetical protein MGC45871	Hs.345588	BC014203	24
BNO700	C7orf30	chromosome 7 open reading frame 30	Hs.87385	NM_138446	24
BNO704	KIAA1102	KIAA1102 protein	Hs.156761	AB029025	
BNO705	BNO705	ESTs	Hs.30280	SEQ ID NO: 13	3
BNO706	LOC116441	hypothetical protein BC014339	Hs.22026	NM_138786	24
BNO708	BNO708	ESTs	Hs.12876	SEQ ID NO: 14	6
BNO710	BNO710	FLJ23228	Hs.170623	AK026881	6
BNO712	BNO712	FLJ21592	Hs.5921	AK025245	3
BNO713	KIAA0970	KIAA0970 protein	Hs.103329	NM_014923	6
BNO714	KIAA0121	KIAA0121 gene product	Hs.155584	D50911	6
BNO723	C14orf123	chromosome 14 open reading frame 123	Hs.279761	NM_014169	6
BNO725	KIAA0582	KIAA0582 protein	Hs.146007	NM_015147	24
BNO730	BNO730	ESTs	Hs.158753	SEQ ID NO: 15	6
BNO731	C6orf166	chromosome 6 open reading frame 166	Hs.201864	NM_018064	3
BNO735	FLJ32029	Unnamed protein product	Hs.26612	NM_173582	6
BNO737	BNO737	hypothetical protein DKFZp434F0318	Hs.23388	NM_030817	
BNO740	KIAA1728	KIAA1728 protein	Hs.437362	AB051515	24
BNO742	BNO742	hypothetical protein FLJ11795	Hs.84560	NM_024669	24
BNO745	BNO745	hypothetical protein DKFZp547A023	Hs.374649	NM_018704	6

TABLE 1 (Continued)

Novel Angiogenesis Genes

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO747	MGC23937	hypothetical protein MGC23937 similar to CG4798	Hs.91612	NM_145052	6
BNO753	BNO753	cDNA DKFZp667P1024	Hs.127811	AL832835	3
BNO754	KIAA0303	KIAA0303 protein	Hs.212787	AB002301	3
BNO756	BNO756	ESTs	Hs.443155	SEQ ID NO: 16, 54	
BNO759	KIAA1416	KIAA1416 protein	Hs.397426	AB037837	6
BNO761	C7orf24	chromosome 7 open reading frame 24	Hs.444840	NM_024051	6
BNO762	FLJ11223	cDNA FLJ11223	Hs.92308	AL832083	3
BNO768	FLJ30478	cDNA FLJ30478	Hs.298258	AK092048	6
BNO772	FLJ10525	Hypothetical protein FLJ10525	Hs.31082	NM_018126	6
BNO780	LOC58489	hypothetical protein from EUROIMAGE 588495	Hs.26765	AL390079	3
BNO782	MGC26717	Hypothetical protein	Hs.406060	BC024188	6
BNO791	KIAA1053	KIAA1053 protein	Hs.98259	NM_015589	6
BNO793	KIAA0766	KIAA0766 gene product	Hs.28020	NM_014805	24
BNO795	BNO795	ESTs moderately similar to MDC-3.13 isoform 2 mRNA	Hs.306343	AK123281	6
BNO800	KIAA1577	KIAA1577 protein	Hs.449290	AB046797	6
BNO802	KIAA0877	KIAA0877 protein	Hs.408623	AB020684	24
BNO812	KIAA0372	KIAA0372 gene product	Hs.435330	NM_014639	6
BNO816	BNO816	cDNA clone 4052238	Hs.348514	BC014384	6
BNO818	MGC10067	hypothetical protein MGC10067	Hs.42251	NM_145049	3
BNO819	KIAA1191	KIAA1191 protein	Hs.8594	NM_020444	24
BNO821	BNO821	ESTs	Hs.87606	SEQ ID NO: 17	24
BNO825	FBXO30	F-box protein 30	Hs.421095	NM_032145	3
BNO831	C8orf1	chromosome 8 open reading frame 1	Hs.436445	NM_004337	24
BNO833	C6orf115	Chromosome 6 open reading frame 115	Hs.238205	BC014953	24
BNO838	BNO838	ESTs	Hs.319095	SEQ ID NO: 18	3
BNO845	FLJ23728	cDNA FLJ23728	Hs.191094	AK074308	6
BNO848	C10orf45	Chromosome 10 open reading frame 45	Hs.103378	NM_031453	24

TABLE 1 (Continued)

Novel Angiogenesis Genes

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO849	BNO849	cDNA DKFZp434G0972	Hs.106148	AL133577	24
BNO852	CGI-111	CGI-111 protein	Hs.11085	NM_016048	6
BNO856	LOC116068	hypothetical protein LOC116068	Hs.136235	AL832721	24
BNO857	C12orf2	chromosome 12 open reading frame 2	Hs.140821	NM_007211	6
BNO862	BNO862	DKFZP434C212 protein	Hs.287266	AK023841	
BNO868	BNO868	DKFZP566C134 protein	Hs.20237	AB040922	3
BNO870	LOC57228	hypothetical protein from clone 643	Hs.206501	NM_020467	24
BNO871	KIAA1463	KIAA1463 protein	Hs.21104	AB040896	6
BNO873	KIAA1376	KIAA1376 protein	Hs.24684	NM_020801	0.5, 24
BNO876	FLJ10326	hypothetical protein FLJ10326	Hs.262823	NM_018060	24
BNO878	BNO878	hypothetical protein DKFZp761L1417	Hs.270753	NM_152913	6
BNO881	MGC11349	hypothetical protein MGC11349	Hs.288697	NM_025112	6
BNO883	FLJ39541	similar to RIKEN cDNA 9130404H11 gene	Hs.21388	NM_178566	6
BNO886	BNO886	cDNA DKFZp686D04119	Hs.30258	BX537597	6
BNO887	KIAA0648	KIAA0648 protein	Hs.31921	NM_015200	24
BNO890	KIAA1160	KIAA1160 protein	Hs.512661	NM_020701	3
BNO892	C20orf108	chromosome 20 open reading frame 108	Hs.143736	NM_080821	3
BNO894	KIAA0205	KIAA0205 gene product	Hs.528724	NM_014873	6
BNO895	C20orf112	chromosome 20 open reading frame 112	Hs.335142	NM_080616	0.5
BNO898	BNO898	clone IMAGE:5243590	Hs.454832	BC036880	6
BNO905	KIAA1462	KIAA1462 protein	Hs.192726	AB040895	3
BNO906	KIAA1199	KIAA1199 protein	Hs.212584	AB033025	6
BNO908	C15orf12	chromosome 15 open reading frame 12	Hs.513041	NM_018285	
BNO910	BNO910	cDNA DKFZp564F053	Hs.529772	AL049265	6
BNO917	BNO917	hypothetical protein dJ465N24.2.1	Hs.259412	NM_020317	24
BNO926	KIAA1238	KIAA1238 protein	Hs.372288	AB033064	
BNO928	BNO928	EST	None	SEQ ID NO: 19	3

TABLE 1 (Continued)

Novel Angiogenesis Genes

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO929	BNO929	EST	None	SEQ ID NO: 20	6
BNO930	BNO930	EST	Hs.478376	SEQ ID NO: 21	6
BNO932	BNO932	EST	Hs.492501	SEQ ID NO: 22, 55	3
BNO933	BNO933	EST	None	SEQ ID NO: 23	6
BNO934	BNO934	EST	None	SEQ ID NO: 24	6
BNO935	BNO935	EST	None	SEQ ID NO: 25	6
BNO936	BNO936	EST	None	SEQ ID NO: 26, 56	6
BNO937	BNO937	alpha gene sequence	None	AF203815	6
BNO938	BNO938	EST	None	SEQ ID NO: 27	0.5
BNO939	BNO939	EST	None	SEQ ID NO: 28	6
BNO940	BNO940	EST	None	SEQ ID NO: 29	6
BNO941	BNO941	EST	None	SEQ ID NO: 30	3
BNO942	BNO942	EST	None	SEQ ID NO: 31	6
BNO943	BNO943	EST	None	SEQ ID NO: 32	6
BNO944	BNO944	EST	None	SEQ ID NO: 33	6
BNO945	BNO945	EST	None	SEQ ID NO: 34	6
BNO946	BNO946	EST	None	SEQ ID NO: 35, 57	6
BNO948	BNO948	EST	None	SEQ ID NO: 36	6
BNO949	BNO949	EST	None	SEQ ID NO: 37, 58	3
BNO950	BNO950	EST	None	SEQ ID NO: 38	24
BNO951	BNO951	EST	None	SEQ ID NO: 39	24
BNO953	BNO953	EST	None	SEQ ID NO: 40	24
BNO961	BNO961	FLJ00138 protein	Hs.199749	AK074067	3, 24
BNO1018	BNO1018	EST	Hs.485935	SEQ ID NO: 41	3
BNO1019	BNO1019	EST	None	SEQ ID NO: 42	24
BNO1020	BNO1020	EST	None	SEQ ID NO: 43	3
BNO1021	BNO1021	EST	None	SEQ ID NO: 44	3

TABLE 2

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO436	NP	nucleoside phosphorylase	Hs.75514	NM_000270	6
BNO438	CD59	CD59 antigen p18-20	Hs.278573	NM_000611	24
BNO441	BIRC3	baculoviral IAP repeat-containing 3	Hs.127799	NM_001165	3
BNO442	FABP5	fatty acid binding protein 5 (psoriasis-associated)	Hs.408061	NM_001444	24
BNO443	CBFB	core-binding factor, beta subunit	Hs.179881	NM_001755	6
BNO446	INHBA	inhibin, beta A (activin A, activin AB alpha polypeptide)	Hs.727	NM_002192	6
BNO447	MGST2	microsomal glutathione S-transferase 2	Hs.81874	NM_002413	24
BNO448	RAB6A	RAB6A, member RAS oncogene family	Hs.5636	NM_002869	6
BNO449	SAT	spermidine/spermine N1-acetyltransferase	Hs.28491	NM_002970	6
BNO451	TXNRD1	thioredoxin reductase 1	Hs.13046	NM_003330	6
BNO452	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	Hs.132904	NM_003615	6
BNO453	PPAP2B	phosphatidic acid phosphatase type 2B	Hs.432840	NM_003713	3
BNO454	BCL10	B-cell CLL/lymphoma 10	Hs.193516	NM_003921	3
BNO455	DUSP1	dual specificity phosphatase 1	Hs.171695	NM_004417	0.5
BNO456	KIF5B	kinesin family member 5B	Hs.149436	NM_004521	6
BNO457	WTAP	Wilms' tumour 1-associating protein	Hs.119	NM_004906	0.5
BNO459	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647	NM_005252	0.5
BNO460	GATA6	GATA binding protein 6	Hs.50924	NM_005257	3
BNO461	HRY	hairy and enhancer of split 1, (Drosophila)	Hs.250666	NM_005524	0.5
BNO462	SGK	serum/glucocorticoid regulated kinase	Hs.296323	NM_005627	3
BNO463	TIEG	TGFB inducible early growth response	Hs.82173	NM_005655	0.5
BNO464	BCAP31	B-cell receptor-associated protein 31	Hs.381232	NM_005745	
BNO465	CALCRL	calcitonin receptor-like	Hs.152175	NM_005795	24
BNO466	SUI1	putative translation initiation factor	Hs.150580	NM_005801	3
BNO467	TSC22	transforming growth factor beta-stimulated protein TSC-22	Hs.114360	NM_006022	6
BNO468	RAN	RAN, member RAS oncogene family	Hs.426035	NM_006325	
BNO469	LYPLA1	lysophospholipase I	Hs.12540	NM_006330	6

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO470	SSFA2	sperm specific antigen 2	Hs.351355	NM_006751	6
BNO472	CLIC4	chloride intracellular channel 4	Hs.25035	NM_013943	24
BNO473	SLC7A11	solute carrier family 7, member 11	Hs.6682	NM_014331	3
BNO474	RAI14	retinoic acid induced 14	Hs.15165	NM_015577	6
BNO475	HSPC014	chromosome 13 open reading frame 12	Hs.279813	NM_015932	24
BNO476	UMP-CMPK	UMP-CMP kinase	Hs.11463	NM_016308	3
BNO477	SLC38A2	solute carrier family 38, member 2	Hs.298275	NM_018976	3
BNO478	ZNF317	zinc finger protein 317	Hs.18587	NM_020933	24
BNO479	RAB6C	RAB6C, member RAS oncogene family	Hs.333139	NM_032144	24
BNO480	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	Hs.142838	NM_032390	3
BNO481	KPNA4	karyopherin alpha 4 (importin alpha 3)	Hs.288193	NM_002268	3
BNO483	C14orf32	chromosome 14 open reading frame 32	Hs.406401	NM_144578	3
BNO484	SMARCA2	SWI/SNF related, matrix associated, regulator of chromatin, A2	Hs.198296	NM_003070	0.5
BNO485	SOX4	Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA	Hs.83484	NM_003107	3
BNO487	NR4A3	nuclear receptor subfamily 4, group A, member 3	Hs.80561	NM_006981	0.5
BNO488	NTN4	netrin 4	Hs.102541	NM_021229	
BNO489	DNCI2	dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA	Hs.66881	XM_027780	0.5
BNO490	UGCG	UDP-glucose ceramide glucosyltransferase	Hs.432605	NM_003358	0.5, 24
BNO491	P125	Sec23-interacting protein p125	Hs.300208	NM_007190	3
BNO492	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	Hs.355399	NM_019094	6
BNO495	SATB1	special AT-rich sequence binding protein 1	Hs.74592	NM_002971	6
BNO496	BZW1	basic leucine zipper and W2 domains 1	Hs.155291	NM_014670	3
BNO497	TDG	thymine-DNA glycosylase	Hs.173824	NM_003211	6
BNO498	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	Hs.380096	NM_005721	24
BNO499	LAMP2	lysosomal-associated membrane protein 2	Hs.8262	NM_013995	6
BNO500	ERBB2IP	erbb2 interacting protein	Hs.8117	NM_018695	6
BNO501	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	Hs.181195	NM_005494	3

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO502	EMP1	epithelial membrane protein 1	Hs.79368	NM_001423	6
BNO503	MAPK1	mitogen-activated protein kinase 1	Hs.324473	NM_002745	24
BNO504	CYP1A1	cytochrome P450, subfamily 1, polypeptide 1	Hs.72912	NM_000499	6
BNO505	ACVR1	activin A receptor, type I	Hs.150402	NM_001105	3
BNO506	TPT1	tumor protein, translationally-controlled 1	Hs.401448	NM_003295	0.5, 24
BNO507	VAV3	vav 3 oncogene	Hs.267659	NM_006113	3
BNO508	CAP	adenylyl cyclase-associated protein	Hs.104125	NM_006367	24
BNO509	HSPA5	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	Hs.75410	NM_005347	6
BNO510	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	Hs.239489	NM_022173	6
BNO511	CCNT2	cyclin T2	Hs.155478	NM_001241	6
BNO512	CHC1L	chromosome condensation 1-like	Hs.27007	NM_001268	0.5
BNO513	SFPQ	splicing factor proline/glutamine rich	Hs.180610	NM_005066	3
BNO514	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha	Hs.183037	NM_002734	24
BNO515	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	Hs.6906	NM_005402	6
BNO516	ANXA2	annexin A2	Hs.217493	NM_004039	0.5
BNO517	NUP153	nucleoporin 153kDa	Hs.211608	NM_005124	3
BNO518	RANBP9	RAN binding protein 9	Hs.279886	NM_005493	24
BNO519	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Hs.198891	NM_003913	6
BNO520	TSN	translin	Hs.75066	NM_004622	6
BNO521	H3F3A	H3 histone, family 3A	Hs.181307	NM_002107	24
BNO523	PROS1	protein S (alpha)	Hs.64016	NM_000313	6
BNO524	DDX3	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	Hs.380774	NM_001356	3
BNO525	TCF4	transcription factor 4	Hs.359289	NM_003199	6
BNO526	PTP4A1	Protein tyrosine phosphatase type IVA, member 1	Hs.227777	NM_003463	6
BNO527	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	Hs.53250	NM_001204	3
BNO528	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	Hs.155396	NM_006164	3
BNO531	AHR	aryl hydrocarbon receptor	Hs.170087	NM_001621	3

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO532	RANBP7	RAN binding protein 7	Hs.5151	NM_006391	3
BNO533	ARF6	ADP-ribosylation factor 6	Hs.89474	NM_001663	3
BNO534	SCARF1	SCARF1 Scavenger receptor class F, member 1	Hs.57735	NM_003693Ê	24
BNO535	PLU-1	putative DNA/chromatin binding motif	Hs.143323	NM_006618	24
BNO536	TOMM20	translocase of outer mitochondrial membrane 20 (yeast) homolog	Hs.75187	NM_014765	6
BNO537	B2M	beta-2-microglobulin	Hs.48516	NM_004048	24
BNO538	zizimin1	zizimin1	Hs.8021	NM_015296	6
BNO539	ARPP-19	cyclic AMP phosphoprotein, 19 kD	Hs.7351	NM_006628	3
BNO540	RAP1B	RAP1B, member of RAS oncogene family	Hs.156764	NM_015646	3
BNO541	MCP	membrane cofactor protein	Hs.83532	NM_153826	6
BNO542	IFI16	interferon, gamma-inducible protein 16	Hs.155530	NM_005531	0.5
BNO543	PRG1	proteoglycan 1, secretory granule	Hs.1908	NM_002727	
BNO544	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	Hs.81665	NM_000222	0.5, 24
BNO545	SYBL1	synaptobrevin-like 1	Hs.24167	NM_005638	6
BNO546	TCF8	transcription factor 8 (represses interleukin 2 expression)	Hs.232068	NM_030751Ê	6
BNO548	NXF1	nuclear RNA export factor 1	Hs.323502	NM_006362	3, 24
BNO549	RAP2B	RAP2B, member of RAS oncogene family	Hs.239527	NM_002886	3
BNO551	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	Hs.82065	NM_002184	6
BNO552	REST	RE1-silencing transcription factor	Hs.401145	NM_005612	6
BNO553	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	Hs.30246	NM_006996	3
BNO554	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	Hs.183684	NM_001418	3
BNO555	PTPRE	protein tyrosine phosphatase, receptor type, E	Hs.31137	NM_006504	3
BNO556	PDE3A	phosphodiesterase 3A, cGMP-inhibited	Hs.777	NM_000921	3
BNO557	C1QR1	complement component 1, q subcomponent, receptor 1	Hs.97199	NM_012072	24
BNO558	RANBP2	RAN binding protein 2	Hs.199179	NM_006267	
BNO559	KIS	kinase interacting with leukemia-associated gene (stathmin)	Hs.127310	NM_144624	24
BNO560	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hs.11899	NM_000859	6

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO561	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	Hs.326248	NM_145341	3
BNO562	TACC1	transforming, acidic coiled-coil containing protein 1	Hs.173159	NM_006283	0.5
BNO564	DIS3	mitotic control protein dis3 homolog	Hs.323346	NM_014953	6
BNO565	TOP2A	topoisomerase (DNA) II alpha 170kDa	Hs.156346	NM_001067	6
BNO566	SLC7A2	solute carrier family 7, member 2	Hs.153985	NM_003046	6
BNO567	FH	fumarate hydratase	Hs.75653	NM_000143	6
BNO568	IL1RL1	interleukin 1 receptor-like 1	Hs.66	NM_003856	6
BNO569	HPRP3P	U4/U6-associated RNA splicing factor	Hs.11776	NM_004698	6
BNO570	DDX5	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5	Hs.76053	NM_004396	
BNO571	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	Hs.79078	NM_002358	0.5, 24
BNO572	MADH7	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	Hs.100602	NM_005904	3
BNO573	E2F3	E2F transcription factor 3	Hs.1189	NM_001949	3
BNO574	CSNK2A2	CSNK2A2 Casein kinase 2, alpha prime polypeptide	Hs.82201	NM_001896	6
BNO575	MAX	MAX protein	Hs.42712	NM_002382	6
BNO576	ERAP140	140 kDa estrogen receptor associated protein	Hs.339283	AF493978	3
BNO577	CD9	CD9 antigen (p24)	Hs.1244	NM_001769	24
BNO578	ATRX	alpha thalassemia/mental retardation syndrome X-linked	Hs.96264	NM_000489	6
BNO579	YWHAZ	tyrosine/tryptophan activation protein, zeta polypeptide	Hs.75103	NM_003406	3
BNO580	IDS	iduronate 2-sulfatase (Hunter syndrome)	Hs.172458	NM_000202	24
BNO581	SERPINE2	serine (or cysteine) proteinase inhibitor, clade E, member 2	Hs.21858	NM_006216	6
BNO582	DDEF1	development and differentiation enhancing factor 1	Hs.10669	NM_018482	6
BNO583	GLRX	glutaredoxin (thioltransferase)	Hs.28988	NM_002064	24
BNO584	MAP3K1	MAP3K1 Mitogen-activated protein kinase kinase kinase 1	Hs.170610	XM_042066	3
BNO585	ANKH	ankylosis, progressive homolog (mouse)	Hs.168640	NM_054027	3
BNO586	RBX1	ring-box 1	Hs.279919	NM_014248	24
BNO587	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	Hs.107474	NM_005966	3
BNO588	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	Hs.83429	NM_003810	3

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO589	PRDX3	peroxiredoxin 3	Hs.75454	NM_006793	6
BNO590	MAP2K1	mitogen-activated protein kinase kinase 1	Hs.3446	NM_002755	3
BNO591	NFATC1	nuclear factor of activated T-cells, calcineurin-dependent 1	Hs.96149	NM_006162	24
BNO594	USP7	ubiquitin specific protease 7 (herpes virus-associated)	Hs.78683	NM_003470	
BNO595	ARHB	ras homolog gene family, member B	Hs.406064	NM_004040	3
BNO596	PTEN	phosphatase and tensin homolog	Hs.10712	NM_000314	
BNO597	UBL1	ubiquitin-like 1 (sentrin)	Hs.81424	NM_003352	24
BNO598	RAB5A	RAB5A, member RAS oncogene family	Hs.73957	NM_004162	3
BNO599	ITGB1	integrin, beta 1	Hs.287797	NM_002211	24
BNO600	PRDM2	PR domain containing 2, with ZNF domain	Hs.26719	NM_012231	6
BNO602	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	Hs.271986	NM_002203	6
BNO603	ETV5	ets variant gene 5 (ets-related molecule)	Hs.43697	NM_004454	3
BNO604	ZFHX1B	zinc finger homeobox 1b	Hs.34871	NM_014795	3
BNO606	LOC157713	lysophospholipase I-like pseudogene on chromosome 6	None	NG_001063	
BNO607	RBM3	RNA binding motif protein 3	Hs.301404	NM_006743	0.5
BNO609	NET-6	transmembrane 4 superfamily member tetraspan NET-6	Hs.364544	NM_014399	6
BNO610	EHD3	EH-domain containing 3	Hs.87125	NM_014600	24
BNO611	KIAA0992	palladin	Hs.194431	NM_016081	6
BNO613	METL	methyltransferase like 2	Hs.433213	NM_018396	3
BNO614	HT010	uncharacterized hypothalamus protein HT010	Hs.6375	NM_018471	0.5
BNO615	C3orf4	chromosome 3 open reading frame 4	Hs.107393	NM_019895	6
BNO619	RPL27A	ribosomal protein L27a	Hs.76064	NM_000990	6
BNO621	MIB	Ubiquitin ligase mind bomb	Hs.34892	AY149908	0.5
BNO623	KIAA0261	KIAA0261 protein	Hs.154978	XM_042946	24
BNO624	KIAA1199	KIAA1199 protein	Hs.50081	XM_051860	6
BNO625	HIF1	huntingtin interacting protein B	Hs.6947	NM_014159	
BNO642	ETL	EGF-TM7-latrophilin-related protein	Hs.57958	NM_022159	24

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO643	VMP1	likely ortholog of rat vacuole membrane protein 1	Hs.166254	NM_030938	3
BNO644	TAF9	TATA box binding protein (TBP)-associated factor, 32kDa	Hs.60679	NM_016283	24
BNO646	MAN1A1	mannosidase, alpha, class 1A, member 1	Hs.432931	NM_005907	6
BNO647	DOCK4	Dedicator of cytokinesis 4	Hs.118140	NM_014705	24
BNO649	ADAMTS9	a disintegrin-like and metalloprotease (thrombospondin type 1 motif, 9)	Hs.126855	NM_020249	24
BNO650	CSNK2A2	Casein kinase 2, alpha prime polypeptide	Hs.82201	NM_001896	6
BNO651	RPLP0	ribosomal protein, large, P0	Hs.406511	NM_001002	6
BNO653	GALNT4	N-acetylgalactosaminyltransferase 4	Hs.271923	NM_003774	3
BNO654	GNG2	guanine nucleotide binding protein (G protein), gamma 2	Hs.289026	BC020774	6
BNO656	MBNL	muscleblind-like (Drosophila)	Hs.28578	NM_021038	
BNO657	ARL8	ADP-ribosylation factor-like 8	Hs.25362	BC024163	3
BNO658	ASB3	ankyrin repeat and SOCS box-containing 3	Hs.9893	NM_016115	6
BNO660	GG2-1	TNF-induced protein	Hs.17839	NM_014350	3
BNO661	ELL2	ELL-related RNA polymerase II, elongation factor	Hs.98124	NM_012081	3
BNO663	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f 2	Hs.235557	NM_004889	24
BNO665	SDCBP	syndecan binding protein (syntenin)	Hs.8180	NM_005625	3
BNO666	KIAA1959	Nm23-phosphorylated unknown substrate	Hs.55067	NM_032873	3
BNO667	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	Hs.478025	NM_198066	6
BNO668	SPRED1	Sprouty-related, EVH1 domain containing 1	Hs.132804	NM_152594	3, 24
BNO670	Nbak2	homeodomain interacting protein kinase 1-like protein	Hs.12259	NM_152696	6
BNO672	GABPA	GA binding protein transcription factor, alpha subunit 60kDa	Hs.78	NM_002040	3
BNO674	V-1	likely ortholog of rat V-1 protein	Hs.21321	NM_145808	24
BNO676	C8FW	phosphoprotein regulated by mitogenic pathways	Hs.7837	NM_025195	3
BNO678	TBC1D4	TBC1 domain family, member 4	Hs.173802	NM_014832	6
BNO679	ACATE2	likely ortholog of mouse acyl-Coenzyme A thioesterase 2	Hs.18625	NM_012332	24
BNO680	CRYZ	crystallin, zeta (quinone reductase)	Hs.83114	NM_001889	6
BNO681	KPNB1	karyopherin (importin) beta 1	Hs.180446	NM_002265	24
BNO682	RPL23A	ribosomal protein L23a	Hs.350046	NM_000984	0.5

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO683	LIMS1	LIM and senescent cell antigen-like domains 1	Hs.112378	NM_004987	6
BNO684	WW45	WW45 protein	Hs.288906	NM_021818	3
BNO686	ST3GALVI	alpha2,3-sialyltransferase	Hs.34578	NM_006100	6
BNO688	CPR8	cell cycle progression 8 protein	Hs.283753	NM_004748	24
BNO689	HDCL	hHDC for homolog of Drosophila headcase	Hs.6679	NM_016217	3
BNO691	UBC	ubiquitin C	Hs.183704	NM_021009	3
BNO692	RDX	radixin	Hs.263671	NM_002906	24
BNO693	PELI1	pellino homolog 1 (Drosophila)	Hs.7886	NM_020651	3
BNO695	MCC	mutated in colorectal cancers	Hs.1345	NM_002387	6
BNO696	RetSDR2	RetSDR2 Retinal short-chain dehydrogenase/reductase 2	Hs.282984	NM_016245	3
BNO698	CSS3	Chondroitin sulfate synthase 3	Hs.165050	AB086062	3
BNO699	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	Hs.80426	NM_004899	6
BNO701	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	Hs.8858	NM_013448	3
BNO702	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	Hs.372673	NM_005463	3
BNO703	PREI3	preimplantation protein 3	Hs.107942	NM_015387	6
BNO707	BNO707	Human XIST, coding sequence "a"	Hs.83623	X56199	3
BNO709	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	Hs.374634	NM_005156	6
BNO711	SMAP-5	golgi membrane protein SB140	Hs.5672	NM_030799	6
BNO715	M-RIP	Myosin phosphatase-Rho interacting protein	Hs.430725	AB020671	0.5, 24
BNO716	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	Hs.75063	NM_006734	3
BNO717	DC42	hypothetical protein DC42	None	NM_030921	3
BNO718	GRPEL2	GrpE-like 2, mitochondrial	Hs.17121	NM_152407	6
BNO719	PCMF	potassium channel modulatory factor	Hs.5392	NM_020122	3
BNO720	UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)	Hs.163546	NM_003341	24
BNO721	KLHL4	kelch-like 4 (Drosophila)	Hs.49075	NM_019117	
BNO722	MANEA	Mannosidase, endo-alpha	Hs.46903	NM_024641	3
BNO724	TCF12	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	Hs.21704	NM_003205	6
BNO726	STAF42	SPT3-associated factor 42	Hs.435967	NM_053053	6

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO727	CYFIP1	cytoplasmic FMR1 interacting protein 1	Hs.77257	NM_014608	6
BNO728	NOL5A	nucleolar protein 5A (56kDa with KKE/D repeat)	Hs.376064	NM_006392	6
BNO729	GSA7	ubiquitin activating enzyme E1-like protein	Hs.278607	NM_006395	6
BNO732	P66 Alpha	P66 Alpha	Hs.118964	NM_017660	
BNO733	STAG1	stromal antigen 1	Hs.286148	NM_005862	
BNO734	MYCT1	Myc target 1	Hs.18160	NM_025107	6
BNO736	SCAMP1	secretory carrier membrane protein 1	Hs.31218	NM_004866	3
BNO738	ACTG1	actin, gamma 1	Hs.14376	NM_001614	0.5
BNO739	HRB2	HIV-1 rev binding protein 2	Hs.154762	NM_007043	6
BNO741	VMP1	Likely orthologue of rat vacuole membrane protein 1	Hs.166254	NM_030938	6
BNO743	BCAT1	branched chain aminotransferase 1, cytosolic	Hs.438993	NM_005504	0.5, 24
BNO744	PJA2	Praja 2, RING-H2 motif containing	Hs.224262	NM_014819	
BNO746	FKSG14	leucine zipper protein FKSG14	Hs.192843	NM_022145	6
BNO748	KLHL6	kelch-like 6 (Drosophila)	Hs.43616	NM_130446	6
BNO749	TTL	Tubulin tyrosine ligase	Hs.358997	NM_153712	6
BNO750	CDC23	CDC23 (cell division cycle 23, yeast, homolog)	Hs.153546	NM_004661	24
BNO751	ULK2	unc-51-like kinase 2 (C. elegans)	Hs.151406	NM_014683	3
BNO752	SCARB2	SCARB2 Scavenger receptor class B, member 2	Hs.323567	NM_005506	3
BNO755	ZMPSTE24	zinc metalloproteinase (STE24 homolog, yeast)	Hs.25846	NM_005857	
BNO757	U5-100K	prp28, U5 snRNP 100 kd protein	Hs.184771	NM_004818	
BNO758	CHD4	chromodomain helicase DNA binding protein 4	Hs.74441	NM_001273	6
BNO760	CGI-127	yippee protein	Hs.184542	NM_016061	3, 24
BNO763	BET1	BET1 homolog (S. cerevisiae)	Hs.23103	NM_005868	24
BNO764	ARHGAP5	Rho GTPase activating protein 5	Hs.267831	NM_001173	
BNO765	TUBA	Scaffold protein TUBA	Hs.429994	NM_015221	3
BNO766	NUMB	numb homolog (Drosophila)	Hs.78890	NM_003744	6
BNO767	P5	protein disulfide isomerase-related protein	Hs.182429	NM_005742	0.5
BNO769	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	Hs.51957	NM_004719	6

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO770	OXA1L	oxidase (cytochrome c) assembly 1-like	Hs.151134	NM_005015	0.5, 24
BNO771	POH1	26S proteasome-associated pad1 homolog	Hs.178761	NM_005805	6
BNO773	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	Hs.4113	NM_006621	3
BNO774	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	Hs.21293	NM_003115	3
BNO775	PLS3	plastin 3 (T isoform)	Hs.4114	NM_005032	6
BNO776	TSNAX	translin-associated factor X	Hs.96247	NM_005999	0.5
BNO777	HELO1	homolog of yeast long chain polyunsaturated fatty acid elong. enz. 2	Hs.250175	NM_021814	6
BNO778	MAN2A1	mannosidase, alpha, class 2A, member 1	Hs.377915	NM_002372	3
BNO779	RAB21	RAB21, member RAS oncogene family	Hs.184627	NM_014999	6
BNO781	WAC	WW domain-containing adapter with a coiled-coil region	Hs.70333	NM_016628	3
BNO783	POSH	likely ortholog of mouse plenty of SH3 domains	Hs.301804	AB040927	6
BNO784	RBM9	RNA binding motif protein 9	Hs.433574	NM_014309	
BNO785	CSRP2	cysteine and glycine-rich protein 2	Hs.10526	NM_001321	3
BNO786	COPA	coatomer protein complex, subunit alpha	Hs.75887	NM_004371	6
BNO787	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	Hs.20716	NM_006335	6
BNO788	RIN2	Ras and Rab interactor 2	Hs.62349	NM_018993	24
BNO789	KLHL5	kelch-like 5 (Drosophila)	Hs.272239	NM_015990	24
BNO790	IPLA2(γ)	intracellular memb.-assoc. calcium-independent phospholipase A2 γ	Hs.44198	AF263613	6
BNO794	SMARCA5	SWI/SNF related regulator of chromatin, a5	Hs.9456	NM_003601	
BNO796	FBXL3A	F-box and leucine-rich repeat protein 3A	Hs.7540	NM_012158	24
BNO797	SART2	squamous cell carcinoma antigen recognized by T cell	Hs.58636	NM_013352Ê	6
BNO798	YWHAZ	14-3-3zeta	Hs.386834	NM_145690	
BNO799	SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	Hs.9167	NM_031469	3, 24
BNO801	PUM1	pumilio homolog 1 (Drosophila)	Hs.153834	NM_014676	3
BNO803	CCT2	chaperonin containing TCP1, subunit 2 (beta)	Hs.432970	NM_006431	6
BNO804	PTPRK	protein tyrosine phosphatase, receptor type, K	Hs.79005	NM_002844	6
BNO806	TM4SF1	transmembrane 4 superfamily member 1	Hs.351316	NM_014220	6
BNO807	CHSY1	carbohydrate (chondroitin) synthase 1	Hs.110488	NM_014918	24

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO808	TERF2IP	telomeric repeat binding factor 2, interacting protein	Hs.274428	NM_018975	6
BNO809	RDC1	G protein-coupled receptor	Hs.23016	BC036661	3
BNO810	CD59	CD59 antigen p18-20	Hs.278573	AK095453	0.5, 6
BNO811	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	Hs.129683	NM_003338	6
BNO813	CUL4B	cullin 4B	Hs.155976	NM_003588	24
BNO814	LCHN	LCHN protein	Hs.233044	AB032973	3
BNO815	PELO	pelota homolog (Drosophila)	Hs.5798	NM_015946	3
BNO817	MRPS10	mitochondrial ribosomal protein S10	Hs.380887	NM_018141	6
BNO820	EIF3S2	eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa	Hs.192023	NM_003757	3
BNO822	UBQLN1	ubiquilin 1	Hs.9589	NM_013438	3
BNO823	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	Hs.82793	NM_002795	0.5, 24
BNO826	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	Hs.184325	NM_016336	24
BNO827	CDK2AP1	CDK2-associated protein 1	Hs.433201	NM_004642	24
BNO828	CRY1	cryptochrome 1 (photolyase-like)	Hs.151573	NM_004075	3
BNO830	HSPC051	ubiquinol-cytochrome c reductase complex (7.2 kD)	Hs.284292	NM_013387	6
BNO832	GNG11	guanine nucleotide binding protein (G protein), gamma 11	Hs.83381	NM_004126	0.5, 24
BNO834	ZNF198	zinc finger protein 198	Hs.109526	NM_003453	6
BNO835	RAB11A	RAB11A, member RAS oncogene family	Hs.75618	NM_004663	6
BNO836	SMAP1	stromal membrane-associated protein	Hs.373517	NM_021940	6
BNO837	COPG	Coatomer protein complex, subunit gamma	Hs.368056	NM_016128	3
BNO839	MTHFD2	methylene tetrahydrofolate dehydrogenase (NAD+ dependent)	Hs.154672	NM_006636	3
BNO840	PODXL	podocalyxin-like	Hs.16426	NM_005397	6
BNO841	SLC30A7	Solute carrier family 30 (zinc transporter), member 7	Hs.38856	NM_133496	3
BNO842	API5	apoptosis inhibitor 5	Hs.227913	NM_006595	3
BNO843	ERdj5	ER-resident protein ERdj5	Hs.1098	NM_018981	3
BNO844	HDGFRP3	Hepatoma-derived growth factor, related protein 3	Hs.127842	NM_016073	6
BNO847	TUCAN	tumor up-regulated CARD-containing antagonist of caspase nine	Hs.10031	NM_014959	6
BNO850	PCDH17	protocadherin 17	Hs.106511	NM_014459	24

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO851	GALNT10	N-acetylgalactosaminyltransferase 10	Hs.107260	NM_017540	24
BNO853	UQCRC1	ubiquinol-cytochrome c reductase core protein I	Hs.119251	NM_003365	6
BNO854	RPL3	ribosomal protein L3	Hs.119598	NM_000967	24
BNO855	CMT2	gene predicted from cDNA with a complete coding sequence	Hs.124	NM_014628	24
BNO858	PSMD7	proteasome 26S subunit, non-ATPase, 7	Hs.155543	NM_002811	6
BNO859	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	Hs.1600	NM_012073	3
BNO860	SEC5	homolog of yeast Sec5	Hs.16580	NM_018303	6
BNO861	SKP1A	S-phase kinase-associated protein 1A (p19A)	Hs.171626	NM_006930	24
BNO863	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	Hs.184270	NM_006135	24
BNO864	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	Hs.194148	NM_005433	24
BNO865	DAAM1	dishevelled associated activator of morphogenesis 1	Hs.197751	NM_014992	6
BNO866	BCL6B	B-cell CLL/lymphoma 6, member B (zinc finger protein)	Hs.22575	NM_181844	6
BNO872	AF5Q31	ALL1 fused gene from 5q31	Hs.231967	NM_014423	6
BNO874	ALDH9A1	aldehyde dehydrogenase 9 family, member A1	Hs.2533	NM_000696	24
BNO875	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	Hs.260024	NM_006449	0.5, 24
BNO877	MIS12	homolog of yeast Mis12	Hs.267194	NM_024039	6
BNO879	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	Hs.272630	NM_015994	6
BNO880	VCIP135	valosin-containing protein (p97)/p47 complex-interacting protein p135	Hs.287727	NM_025054	6
BNO882	D10S170	DNA segment on chromosome 10 (unique) 170	Hs.288862	NM_005436	6
BNO884	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	Hs.293750	NM_005719	24
BNO885	RPS19	ribosomal protein S19	Hs.298262	NM_001022	6
BNO888	NEUGRIN	mesenchymal stem cell protein DSC92	Hs.323467	NM_016645	6
BNO889	CALD1	caldesmon 1	Hs.325474	NM_033138	0.5
BNO891	NFIB	nuclear factor I/B	Hs.33287	NM_005596	0.5
BNO893	HSPCA	heat shock 90kDa protein 1, alpha	Hs.356531	NM_005348	6
BNO896	NSAP1	NS1-associated protein 1	Hs.373499	NM_006372	6
BNO897	SYT11	synaptotagmin XI	Hs.380439	NM_152280	6
BNO899	HNRPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	Hs.406125	NM_006321	24
BNO900	STMN1	stathmin 1/oncoprotein 18	Hs.406269	NM_005563	6

TABLE 2 (Continued)

Genes with a Previously Unknown Role in Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO901	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta	Hs.406510	NM_001686	0.5, 24
BNO902	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	Hs.407981	NM_002793	0.5, 24
BNO903	DDX10	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase)	Hs.41706	NM_004398	6
BNO904	RPL36AL	ribosomal protein L36a-like	Hs.419465	NM_001001	24
BNO907	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	Hs.51299	NM_021074	0.5, 24
BNO909	DCK	deoxycytidine kinase	Hs.709	NM_000788	24
BNO911	MDH1	malate dehydrogenase 1, NAD (soluble)	Hs.75375	NM_005917	24
BNO912	SERP1	stress-associated endoplasmic reticulum protein 1	Hs.76698	NM_014445	0.5
BNO913	RPS3A	ribosomal protein S3A	Hs.77039	NM_001006	0.5
BNO914	ARHA	ras homolog gene family, member A	Hs.77273	NM_001664	0.5
BNO915	LAMA4	laminin, alpha 4	Hs.78672	NM_002290	6
BNO916	SNX9	sorting nexin 9	Hs.7905	NM_016224	6
BNO918	RAD21	RAD21 homolog (S. pombe)	Hs.81848	NM_006265	0.5, 24
BNO920	PHLDA1	pleckstrin homology-like domain, family A, member 1	Hs.82101	NM_007350	6
BNO921	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	Hs.83656	NM_001175	24
BNO922	ELP2	elongator protein 2	Hs.8739	NM_018255	6
BNO924	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1	Hs.90336	NM_004888	24
BNO925	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	Hs.94	NM_001539	3
BNO927	CYB561	cytochrome b-561	None	NM_001915	24
BNO947	HNRPDL	Heterogeneous nuclear ribonucleoprotein D-like	Hs.372673	NM_005463	3
BNO952	ARHB	Ras homolog gene family, member B	Hs.406064	NM_004040	3
BNO955	CYB561	Cytochrome b-561	Hs.355264	AK095244	24
BNO958	ATP6	ATP synthase F0 subunit 6 - mitochondrial gene	None	NC_001807	24
BNO969	ND4L	NADH dehydrogenase subunit 4L - mitochondrial gene	None	NC_001807	6
BNO960	COX2	cytochrome C oxidase subunit II - mitochondrial gene	None	NC_001807	0.5, 24
BNO1014	SET	SET translocation (myeloid leukemia-associated)	Hs.145279	NM_003011	6
BNO1015	JUNB	jun B proto-oncogene	Hs.400124	NM_002229	0.5
BNO1016	HMGB1	high-mobility group box 1	Hs:6727	NM_002128	6
BNO1017	PAFAH1B2	Platelet-activating factor acetylhydrolase, isoform Ib, beta subunit	Hs.93354	NM_002572	24

TABLE 3

Genes Previously Associated with Angiogenesis

BNO Number	Symbol	Gene Description - Homology	UniGene Number	GenBank Number	Peak Expression (h)
BNO435	ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	Hs.168383	NM_000201	3
BNO437	IL8	interleukin 8	Hs.624	NM_000584	3
BNO439	VCAM1	vascular cell adhesion molecule 1	Hs.109225	NM_001078	3
BNO440	ANGPT2	angiopoietin 2	Hs.115181	NM_001147	6
BNO444	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	Hs.171271	NM_001904	3
BNO445	F3	coagulation factor III (thromboplastin, tissue factor)	Hs.62192	NM_001993	3
BNO450	STC1	stanniocalcin 1	Hs.25590	NM_003155	24
BNO458	ADAMTS4	a disintegrin-like and metalloprotease (thrombospondin type 1 motif, 4)	Hs.211604	NM_005099	6
BNO471	ESM1	endothelial cell-specific molecule 1	Hs.41716	NM_007036	3, 24
BNO482	CMG2	capillary morphogenesis protein 2	Hs.5897	NM_058172	6
BNO486	EFNB2	ephrin-B2	Hs.30942	NM_004093	3
BNO493	PTGS1	prostaglandin-endoperoxide synthase 1	Hs.88474	NM_000962	6
BNO494	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	Hs.12337	NM_002253	
BNO522	F2R	coagulation factor II (thrombin) receptor	Hs.128087	NM_001992	3
BNO529	CTSB	cathepsin B	Hs.297939	NM_001908	24
BNO530	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	Hs.2250	NM_002309	3
BNO547	EDN1	endothelin 1	Hs.2271	NM_001955	0.5
BNO550	JAK1	Janus kinase 1 (a protein tyrosine kinase)	Hs.50651	NM_002227	24
BNO563	THBD	thrombomodulin	Hs.2030	NM_000361	24
BNO592	PSEN1	presenilin 1 (Alzheimer disease 3)	Hs.3260	NM_000021	0.5
BNO593	STAT3	signal transducer and activator of transcription 3	Hs.321677	NM_139276	6
BNO601	GJA1	gap junction protein, alpha 1, 43kDa (connexin 43)	Hs.74471	NM_000165	3
BNO608	HEY1	hairy/enhancer-of-split related with YRPW motif 1	Hs.234434	NM_012258	0.5
BNO846	CXCR4	chemokine (C-X-C motif) receptor 4	Hs.89414	NM_003467	24
BNO869	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	Hs.205353	NM_001776	0.5
BNO919	SERPINE1	serine (or cysteine) proteinase inhibitor, clade E, member 1	Hs.82085	NM_000602	3
BNO923	THBS1	thrombospondin 1	Hs.87409	NM_003246	0.5

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Claims

1. A method for the identification of a nucleic acid molecule differentially expressed in an *in vitro* model of a biological system, comprising the steps of:

(1) harvesting cells from the model system at predetermined time points;

(2) obtaining total RNA from the cells harvested at each time point;

(3) preparing cDNA from the total RNA from each time point to provide a plurality of pools of cDNA;

(4) performing a suppression subtractive hybridization (SSH) on the cDNA pools from each time point sequentially so as to progressively amplify cDNAs derived from nucleic acid molecules differentially expressed from one time period to the next.

2. A method as claimed in claim 1 wherein the model system is an *in vitro* model for angiogenesis.

3. A nucleic acid molecule differentially expressed during angiogenesis when identified by the method of claim 1 or claim 2.

4. A nucleic acid molecule as claimed in claim 3 selected from the group consisting of those laid out in Tables 1 and 2.

5. A method for the identification of a nucleic acid molecule up-regulated in an *in vitro* model of a biological system, comprising the steps of:

(1) harvesting cells from the model system at predetermined time points;

(2) obtaining total RNA from the cells harvested at each time point;

(3) preparing cDNA from the total RNA from each time point to provide a plurality of pools of cDNA;

(4) performing a suppression subtractive

hybridization (SSH) on the cDNA pools from each time point sequentially so as to progressively amplify cDNAs derived from nucleic acid molecules differentially expressed from one time period to the next.

(5) cloning the amplified cDNAs;

(6) locating DNA from each clone on a microarray;

(7) generating antisense RNA by reverse transcription of total RNA from cells harvested from the *in vitro* model at said predetermined time intervals and labelling the antisense RNA; and

(8) probing the microarray with labelled antisense RNA from 0 hours and each of the other time points separately to identify clones containing cDNA derived from nucleic acid molecules which are up-regulated at said time points in the *in vitro* model.

6. A method as claimed in claim 5 wherein the *in vitro* model is an *in vitro* model for angiogenesis.

7. A nucleic acid molecule when identified by the method of claim 5 or claim 6.

8. A nucleic acid molecule as claimed in claim 7 selected from the group consisting of those set forth in Tables 1 and 2.

9. A polypeptide encoded by a nucleic acid molecule as claimed in any one of claims 3, 4, 7 or 8.

10. An isolated nucleic acid molecule comprising the sequence set forth in one of SEQ ID Numbers: 1 to 44.

11. An isolated nucleic acid molecule comprising the sequence set forth in one of SEQ ID Numbers: 1 to 44 or as laid out in Tables 1 and 2, or a fragment thereof, and

which encodes a polypeptide that plays a role in an angiogenic process.

12. An isolated nucleic acid molecule that is at least 70% identical to a nucleic acid molecule comprising the sequence set forth in one of SEQ ID Numbers: 1 to 44 or as laid out in Tables 1 and 2, and which encodes a polypeptide that plays a role in an angiogenic process.

13. An isolated nucleic acid molecule as claimed in claim 12 that is at least 85% identical.

14. An isolated nucleic acid molecule as claimed in claim 12 that is at least 95% identical.

15. An isolated nucleic acid molecule that encodes a polypeptide that plays a role in an angiogenic process, and which hybridizes under stringent conditions with a nucleic acid molecule comprising the nucleotide sequence set forth in one of SEQ ID Numbers: 1 to 44 or as laid out in Tables 1 and 2.

16. An isolated nucleic acid molecule as claimed in any one of claims 10 to 15, which encodes a polypeptide that plays a role in diseases associated with angiogenesis including but not restricted to cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis, cardiovascular diseases such as atherosclerosis, ischaemic limb disease and coronary artery disease.

17. An isolated nucleic acid molecule consisting any one of the nucleotide sequences set forth in SEQ ID Numbers: 1 to 44.

18. Use of a nucleic acid molecule selected from the group consisting of DNA molecules having the sequence set forth in SEQ ID Numbers: 1 to 15, 17 to 37, and 39 to 44

to identify and/or obtain full-length human genes involved in an angiogenic process.

19. Use as claimed in claim 18 wherein additional sequence is obtained using hybridization with one or more of said nucleic acid molecules, inverse PCR, restriction site PCR, PCR walking techniques or RACE.

20. A gene when identified by the use of a nucleic acid molecule selected from any one of SEQ ID Numbers: 1 to 15, 17 to 37, and 39 to 44.

21. An isolated polypeptide comprising the sequence set forth in one of SEQ ID Numbers: 51 to 58.

22. An isolated polypeptide comprising the sequence set forth in one of SEQ ID Numbers: 51 to 58 or as laid out in Tables 1 and 2, or a fragment thereof, that plays a role in an angiogenic process.

23. An isolated polypeptide that plays a role in an angiogenic process, and having at least 70% identity with the amino acid sequence set forth in SEQ ID Numbers: 51 to 58 or a gene as laid out in Tables 1 and 2.

24. An isolated polypeptide as claimed in claim 23 with at least 85% sequence identity.

25. An isolated polypeptide as claimed in claim 23 with at least 95% sequence identity.

26. An isolated polypeptide as claimed in any one of claims 21 to 25 that plays a role in diseases associated with an angiogenic process including but not restricted to cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis, cardiovascular diseases such as

atherosclerosis, ischaemic limb disease and coronary artery disease.

27. An isolated polypeptide consisting any one of the amino acid sequences set forth in SEQ ID Numbers: 51 to 58.

28. An expression vector comprising a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

29. A cell comprising an expression vector of claim 28.

30. A cell as claimed in claim 29 which is an eukaryotic cell.

31. A method of preparing a polypeptide comprising the steps of :

(1) culturing cells as claimed in either one of claims 29 or 30 under conditions effective for polypeptide production; and

(2) harvesting the polypeptide.

32. A polypeptide prepared by the method of claim 31.

33. A method of modulating angiogenesis comprising modulating the expression or activity of a polypeptide in a cell, wherein the polypeptide is encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

34. The method of claim 33 wherein the nucleic acid molecule is selected from the group consisting of SEQ ID Numbers: 1 to 44.

35. The method of claim 33 wherein the polypeptide is that which is claimed in any one of claim 9, claims 21 to 27, or claim 32, or an active fragment thereof.

36. The method of claim 35 wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID Numbers: 51 to 58.

37. The method of claim 33 wherein the expression or activity of the polypeptide is modulated by introducing into the cell an antagonist or agonist of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17, or a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32.

38. The method of claim 33 wherein the expression or activity of the polypeptide is modulated by introducing into the cell an antisense to a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

39. The method of claim 33 wherein the expression or activity of the polypeptide is modulated by introducing into the cell a nucleic acid molecule which is the complement of at least a portion of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 and is capable of modulating expression or levels of the nucleic acid molecule.

40. The method of claim 39 wherein the nucleic acid molecule is an RNA molecule that hybridizes with the mRNA encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

41. The method of claim 39 wherein the nucleic acid molecule is a short interfering oligonucleotide that hybridizes with the mRNA encoded by a nucleic acid

molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

42. The method of claim 39 wherein the nucleic acid molecule is a catalytic nucleic acid molecule that is targeted to a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

43. The method of claim 42 wherein the catalytic nucleic acid molecule is a DNAzyme.

44. The method of claim 42 wherein the catalytic nucleic acid molecule is a ribozyme.

45. The method of claim 33 wherein the polypeptide expression or activity is modulated by an antibody capable of binding the polypeptide.

46. The method of claim 45 wherein the antibody is a fully human antibody.

47. The method of claim 45 wherein the antibody is selected from the group consisting of a monoclonal antibody, a humanised antibody, a chimaeric antibody or an antibody fragment including a Fab fragment, $(Fab')_2$ fragment, Fv fragment, single chain antibodies and single domain antibodies.

48. The method of claim 33 wherein the polypeptide expression or activity is modulated by introducing into the cell a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17, or an active fragment or variant thereof.

49. The method of claim 48 wherein the nucleic acid molecule is introduced by way of an expression vector as claimed in claim 28.

50. The method of claim 33 wherein the polypeptide expression or activity is modulated by introducing into the cell a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32.

51. The method of any one of claims 33 to 50 wherein angiogenesis is uncontrolled or enhanced.

52. The method of any one of claims 33 to 50 wherein angiogenesis is inappropriately arrested or decreased.

53. A method for the treatment of an angiogenesis-related disorder, comprising modulating the expression or activity of a polypeptide encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

54. The method of claim 53 wherein the nucleic acid molecule is selected from the group consisting of SEQ ID Numbers: 1 to 44.

55. The method of claim 53 wherein the polypeptide is that which is claimed in any one of claim 9, claims 21 to 27, or claim 32, or an active fragment thereof.

56. The method of claim 55 wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID Numbers: 51 to 58.

57. The method of claim 53 wherein the expression or activity of the polypeptide is modulated by introducing into the cell an antagonist or agonist of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 or an antagonist or agonist of a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32.

58. The method of claim 53 wherein the expression or activity of the polypeptide is modulated by introducing into the cell an antisense to a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

59. The method of claim 53 wherein the expression or activity of the polypeptide is modulated by introducing into the cell a nucleic acid molecule which is the complement of at least a portion of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 and is capable of modulating expression or levels of the nucleic acid molecule.

60. The method of claim 59 wherein the nucleic acid molecule is an RNA molecule that hybridizes with the mRNA encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

61. The method of claim 59 wherein the nucleic acid molecule is a short interfering oligonucleotide that hybridizes with the mRNA encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

62. The method of claim 59 wherein the nucleic acid molecule is a catalytic nucleic acid molecule that is targeted to a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

63. The method of claim 62 wherein the catalytic nucleic acid molecule is a DNAzyme.

64. The method of claim 62 wherein the catalytic nucleic acid molecule is a ribozyme.

65. The method of claim 53 wherein the polypeptide expression or activity is modulated by an antibody capable of binding the polypeptide.

66. The method of claim 65 wherein the antibody is a full human antibody.

67. The method of claim 65 wherein the antibody is selected from the group consisting of a monoclonal antibody, a humanised antibody, a chimaeric antibody or an antibody fragment including a Fab fragment, $(Fab')_2$ fragment, Fv fragment, single chain antibodies and single domain antibodies.

68. The method of claim 53 wherein the polypeptide expression or activity is modulated by introducing into the cell a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17, or an active fragment or variant thereof.

69. The method of claim 68 wherein the nucleic acid molecule is introduced by way of an expression vector as claimed in claim 28.

70. The method of claim 53 wherein the polypeptide expression or activity is modulated by introducing into the cell a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32.

71. The method of any one of claims 53 to 70 wherein the angiogenesis-related disorder involves uncontrolled or enhanced angiogenesisis, or is a disorder in which a decreased vasculature is of benefit.

72. The method of claim 71 wherein the disorder is selected from the group consisting of cancer, rheumatoid

arthritis, diabetic retinopathy, psoriasis and cardiovascular diseases such as atherosclerosis.

73. The method of any one of claims 53 to 70 wherein the angiogenesis-related disorder involves inappropriately arrested or decreased angiogenesisis, or is a disorder in which an expanding vasculature is of benefit.

74. The method of claim 73 wherein the disorder is selected from the group consisting of ischaemic limb disease or coronary artery disease.

75. Use of a modulator of expression or activity of a polypeptide encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 in the manufacture of a medicament for the treatment of an angiogenesis-related disorder.

76. The use of claim 75 wherein the nucleic acid sequence is selected from the group consisting of SEQ ID Numbers: 1 to 44.

77. The use of claim 75 wherein the polypeptide is that which is claimed in any one of claim 9, claims 21 to 27, or claim 32, or an active fragment thereof.

78. The use of claim 77 wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID Numbers: 51 to 58.

79. The use of claim 75 wherein the expression or activity of the polypeptide is modulated by introducing into the cell an antagonist or agonist of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 or an antagonist or agonist of a polypeptide as claimed in any one of claim 9, claims 21 to 27 or claim 32.

80. The use of claim 75 wherein the expression or activity of the polypeptide is modulated by introducing into the cell an antisense to a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

81. The use of claim 75 wherein the expression or activity of the polypeptide is modulated by introducing into the cell a nucleic acid molecule which is the complement of at least a portion of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 and is capable of modulating expression or levels of the nucleic acid molecule.

82. The use of claim 81 wherein the nucleic acid molecule is an RNA molecule that hybridizes with the mRNA encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

83. The use of claim 81 wherein the nucleic acid molecule is a short interfering oligonucleotide that hybridizes with the mRNA encoded by a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

84. The use of claim 81 wherein the nucleic acid molecule is a catalytic nucleic acid molecule that is targeted to a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

85. The use of claim 84 wherein the catalytic nucleic acid molecule is a DNAzyme.

86. The use of claim 84 wherein the catalytic nucleic acid molecule is a ribozyme.

87. The use of claim 75 wherein the polypeptide expression or activity is modulated by an antibody capable of binding the polypeptide.

88. The use of claim 87 wherein the antibody is a full human antibody.

89. The use of claim 87 wherein the antibody is selected from the group consisting of a monoclonal antibody, a humanised antibody, a chimaeric antibody or an antibody fragment including a Fab fragment, $(Fab')_2$ fragment, Fv fragment, single chain antibodies and single domain antibodies.

90. The use of claim 75 wherein the polypeptide expression or activity is modulated by introducing into the cell a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17, or an active fragment or variant thereof.

91. The use of claim 90 wherein the nucleic acid molecule is introduced by way of an expression vector as claimed in claim 28.

92. The use of claim 75 wherein the polypeptide expression or activity is modulated by introducing into the cell a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32.

93. The use of any one of claims 75 to 92 wherein the angiogenesis-related disorder involves uncontrolled or enhanced angiogenesisis, or is a disorder in which a decreased vasculature is of benefit.

94. The use of claim 93 wherein the disorder is selected from the group consisting of cancer, rheumatoid arthritis,

diabetic retinopathy, psoriasis and cardiovascular diseases such as atherosclerosis.

95. The use of any one of claims 75 to 92 wherein the angiogenesis-related disorder involves inappropriately arrested or decreased angiogenesisis, or is a disorder in which an expanding vasculature is of benefit.

96. The use of claim 95 wherein the disorder is selected from the group consisting of ischaemic limb disease or coronary artery disease.

97. The use of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 for the screening of candidate pharmaceutical compounds useful in the treatment of angiogenesis-related disorders.

98. A compound useful in the treatment of angiogenesis-related disorders when identified by the use of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

99. The use of a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32 for the screening of candidate pharmaceutical compounds useful in the treatment of angiogenesis-related disorders.

100. A compound useful in the treatment of angiogenesis-related disorders when identified by the use of a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32.

101. The use of a cell as claimed in either one of claims 29 or 30 for the screening of candidate pharmaceutical compounds useful in the treatment of angiogenesis-related disorders.

102. A compound useful in the treatment of angiogenesis-related disorders when identified by the use of a cell as claimed in either one of claims 29 or 30.

103. A method of screening for a candidate pharmaceutical compound useful in the treatment of angiogenesis-related disorders comprising the steps of:

(1) providing a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32;

(2) adding a candidate pharmaceutical compound to said polypeptide; and

(3) determining the binding of said candidate compound to said polypeptide;

wherein a compound that binds to the polypeptide is a candidate pharmaceutical compound.

104. A method of screening for candidate pharmaceutical compound useful in the treatment of angiogenesis-related disorders comprising the steps of:

(1) providing a cell, as claimed in either one of claims 29 or 30;

(2) adding a candidate pharmaceutical compound to said cell; and

(3) determining the effect of said candidate pharmaceutical compound on the functional properties of said cell;

wherein a compound that alters the functional properties of said cell is a candidate pharmaceutical compound.

105. A method of screening for a candidate pharmaceutical compound useful in the treatment of angiogenesis-related disorders comprising the steps of:

(1) providing a cell, as claimed in either one of claims 29 or 30;

(2) adding a candidate pharmaceutical compound to said cell; and

(3) determining the effect of said candidate pharmaceutical compound on the expression of the nucleic acid molecule that is part of the expression vector in said cell;

wherein a compound that alters the expression of the nucleic acid molecule that is part of the expression vector in said cell is a candidate pharmaceutical compound.

106. A method of screening for a candidate pharmaceutical compound useful in the treatment of angiogenesis-related disorders comprising the steps of:

(1) providing a cell, as claimed in either one of claims 29 or 30;

(2) adding a candidate pharmaceutical compound to said cell; and

(3) determining the effect of said candidate pharmaceutical compound on the expression or activity of the polypeptide encoded by the nucleic acid molecule that is part of the expression vector in said cell;

wherein a compound that alters the expression or activity of polypeptide encoded by the nucleic acid molecule that is part of the expression vector in said cell is a candidate pharmaceutical compound.

107. A compound when identified by the method of any one of claims 103 to 106.

108. A pharmaceutical composition comprising a compound as claimed in any one of claims 98, 100, 102 or 107 and a pharmaceutically acceptable carrier.

109. An antibody which is immunologically reactive with an isolated polypeptide as claimed in claim 21.

110. An antibody as claimed in claim 109 which is a fully human antibody.

111. An antibody as claimed in claim 109 which is selected from the group consisting of a monoclonal antibody, a humanised antibody, a chimaeric antibody or an antibody fragment including a Fab fragment, $(Fab')_2$ fragment, Fv fragment, single chain antibodies and single domain antibodies.

112. A short interfering oligonucleotide targeted to the mRNA encoded by a nucleic acid molecule as claimed in claim 10.

113. A catalytic nucleic acid molecule targeted to a nucleic acid molecule as claimed in claim 10.

114. A catalytic nucleic acid molecule of claim 113 which is a DNAzyme.

115. A catalytic nucleic acid molecule of claim 113 which is a ribozyme.

116. Use of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17 in the diagnosis or prognosis of an angiogenesis-related disorder.

117. Use of a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32 in the diagnosis or prognosis of an angiogenesis-related disorder.

118. Use of an antibody as claimed in any one of claims 109 to 111 or an antibody to a polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32 in the diagnosis or prognosis of an angiogenesis-related disorder.

119. A method for the diagnosis or prognosis of an angiogenesis-related disorder comprising the steps of:

(1) establishing a profile for normal expression and/or activity of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17, in unaffected subjects;

(2) measuring the level of expression and/or activity of said nucleic acid molecule in a person suspected of abnormal expression and/or activity of the gene; and

(3) comparing the measured level of expression and/or activity of said nucleic acid molecule with the profile for normal expression and/or activity;

wherein an altered level of expression and/or activity of said nucleic acid molecule in said subject is an indication of an angiogenesis-related disorder, or a predisposition thereto.

120. A method as claimed in claim 119 wherein reverse-transcriptase PCR is employed to measure levels of expression.

121. A method as claimed in claim 119 wherein a hybridization assay using a probe derived from the gene, or a fragment thereof, is employed to measure levels of expression.

122. A method for the diagnosis or prognosis of an angiogenesis-related comprising the steps of:

(1) obtaining DNA from a subject corresponding to a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17; and

(2) comparing the DNA from said subject to the DNA of the corresponding wild-type nucleic acid molecule;

wherein altered DNA properties in said subject is an indication of an angiogenesis-related disorder, or a predisposition thereto.

123. A method as claimed in claim 122 wherein the DNA of the nucleic acid molecule is sequenced and the sequences compared.

124. A method as claimed in claim 122 wherein the DNA of the nucleic acid molecule is subjected to SSCP analysis.

125. A method for the diagnosis or prognosis of an angiogenesis-related disorder comprising the steps of:

(1) establishing a physical property of a wild-type polypeptide as claimed in any one of claim 9, claims 21 to 27, or claim 32;

(2) obtaining the polypeptide from a person suspected of an abnormality of that polypeptide; and;

(3) measuring the property for the polypeptide expressed by said person and comparing it to the established property for the wild-type polypeptide;

wherein altered polypeptide properties in said subject is an indication of an angiogenesis-related disorder, or a predisposition thereto.

126. A method as claimed in claim 125 wherein the property is the electrophoretic mobility.

127. A method as claimed in claim 125 wherein the property is the proteolytic cleavage pattern.

128. A genetically modified non-human animal comprising a isolated a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

129. A genetically modified non-human animal comprising a disruption of a nucleic acid molecule as claimed in any one of claims 3 to 4, claims 7 to 8, or claims 10 to 17.

130. A genetically modified non-human animal as claimed in either one of claims 128 or 129 in which the animal is selected from the group consisting of rats, mice, hamsters, guinea pigs, rabbits, dogs, cats, goats, sheep, pigs and non-human primates such as monkeys and chimpanzees.

131. A genetically modified non-human animal as claimed in any one of claims 128 to 130 wherein the animal is a mouse.

132. Use of a genetically modified non-human animal as claimed in any one of claims 128 to 131 in screening for candidate pharmaceutical compounds useful for the treatment of angiogenesis-related disorders.

133. The use of any one of claims 97 to 102 or claim 132 wherein the angiogenesis-related disorder involves uncontrolled or enhanced angiogenesis, or is a disorder in which a decreased vasculature is of benefit.

134. The use of claim 133 wherein the disorder is selected from the group consisting of cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis and cardiovascular diseases such as atherosclerosis.

135. The use of any one of claims 97 to 102 or claim 132 wherein the angiogenesis-related disorder involves inappropriately arrested or decreased angiogenesis, or is

a disorder in which an expanding vasculature is of benefit.

136. The use of claim 135 wherein the disorder is selected from the group consisting of ischaemic limb disease or coronary artery disease.

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Figure 1

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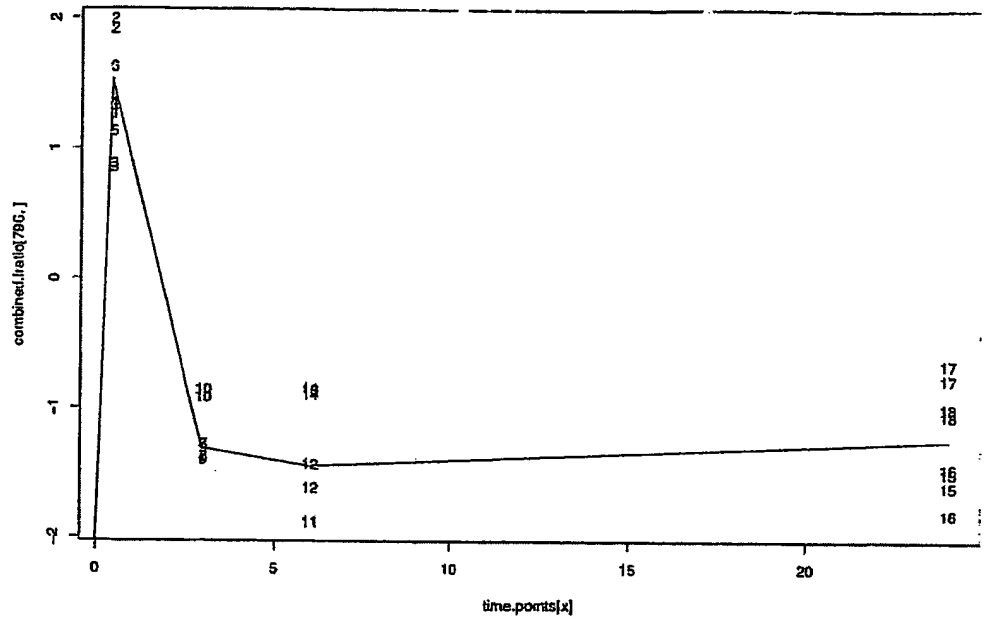

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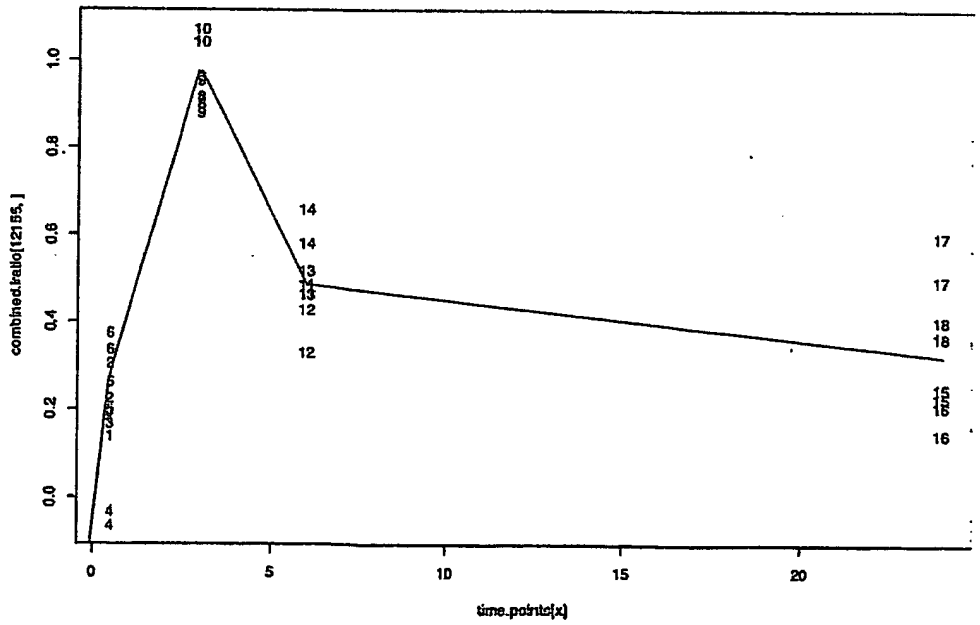

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Figure 1 (Continued)

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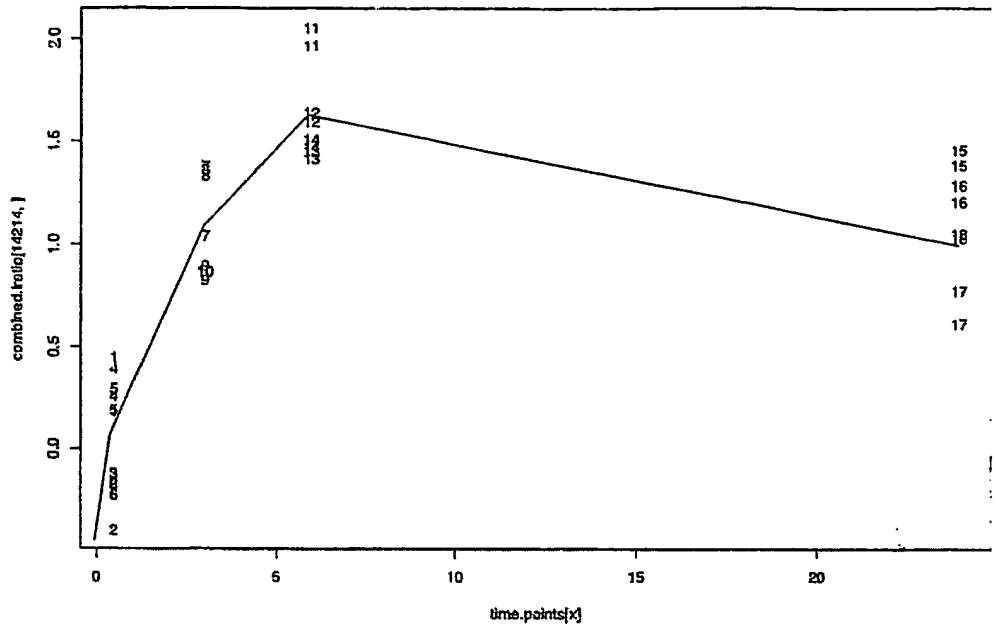

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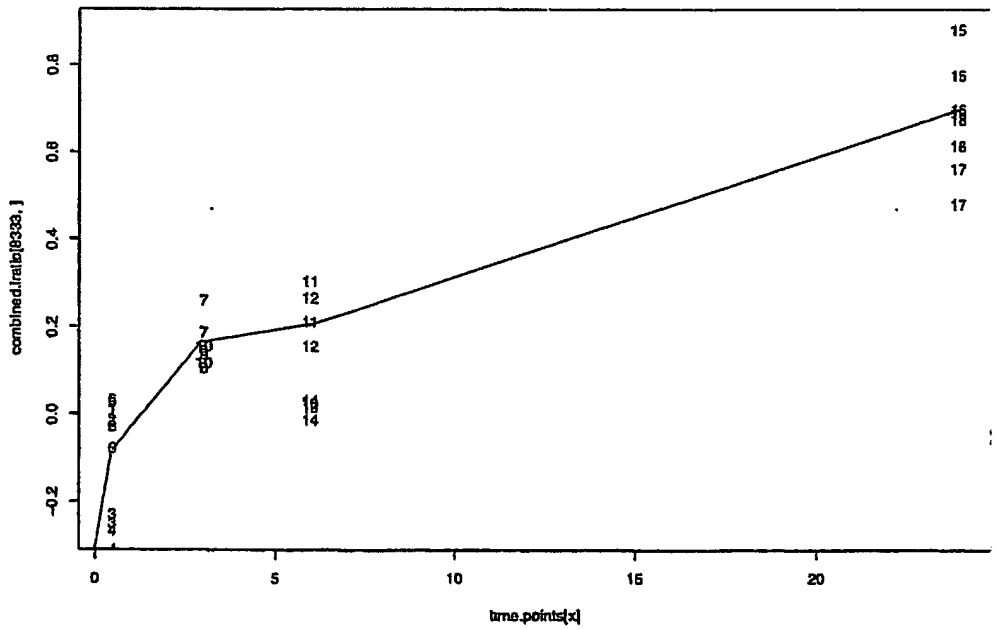

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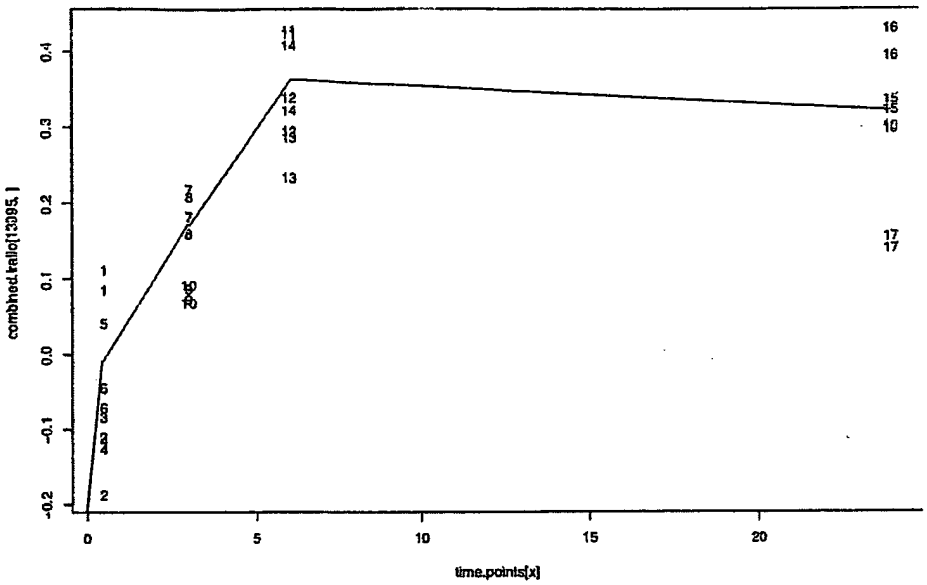
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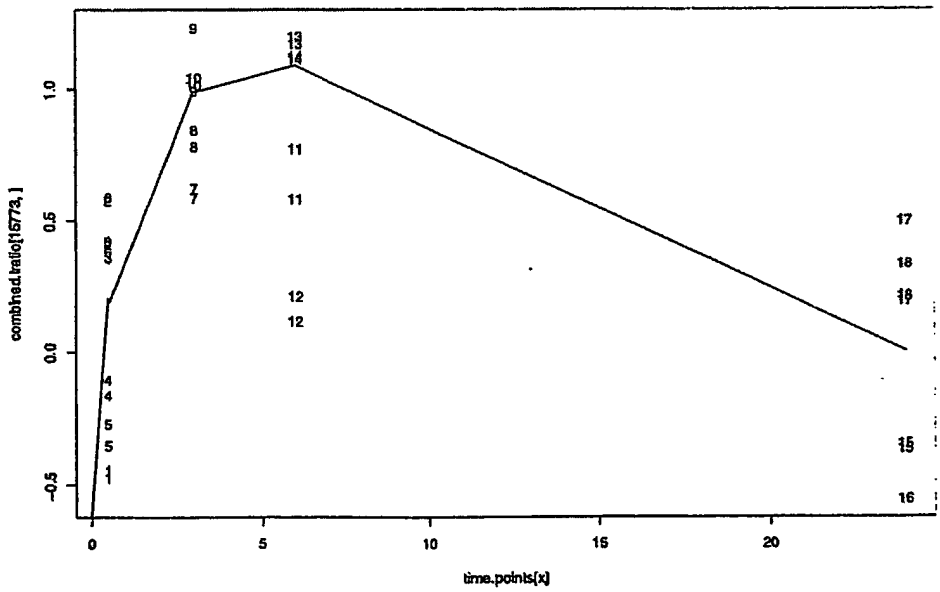
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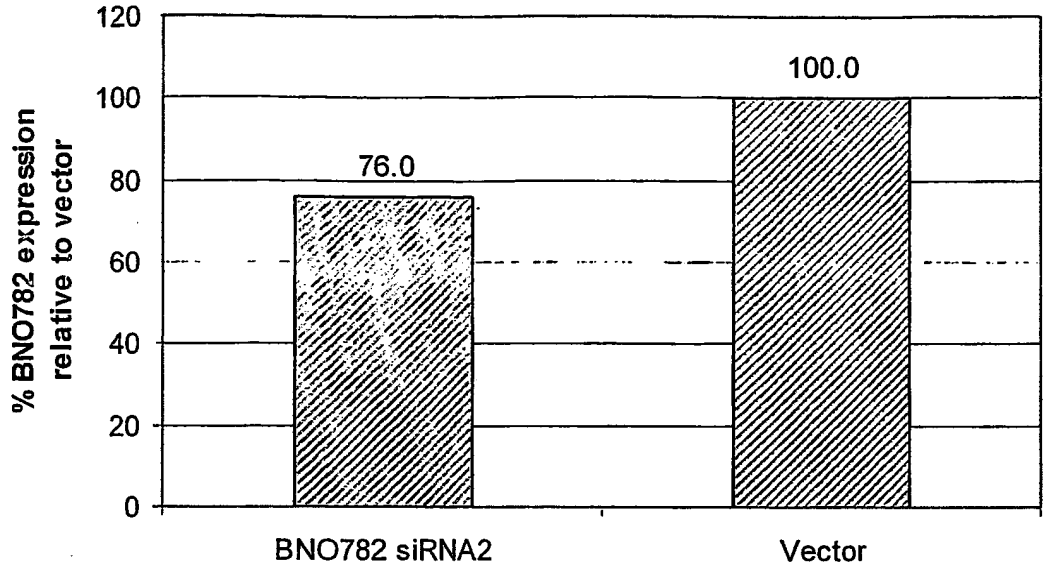
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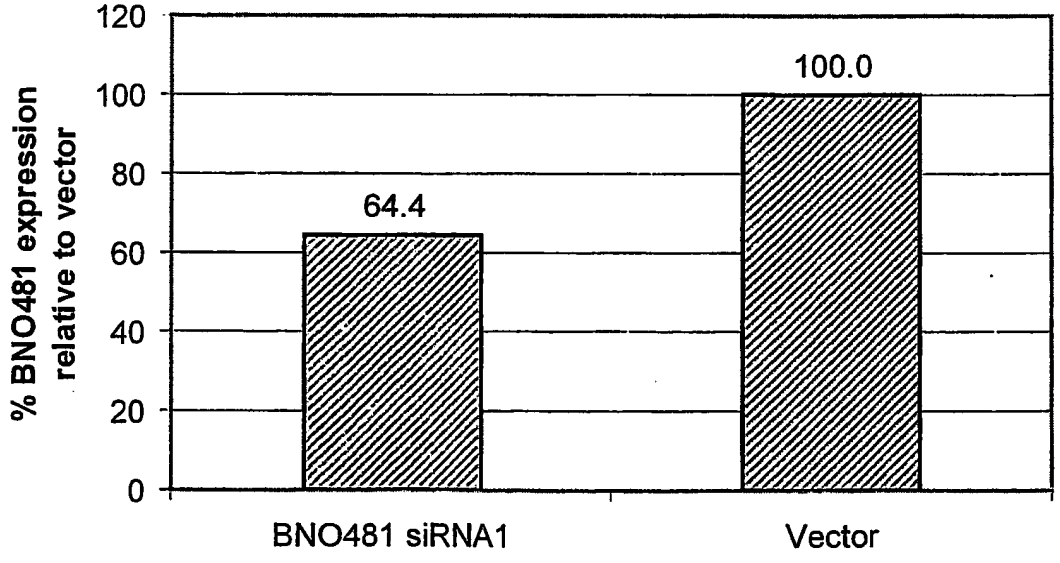
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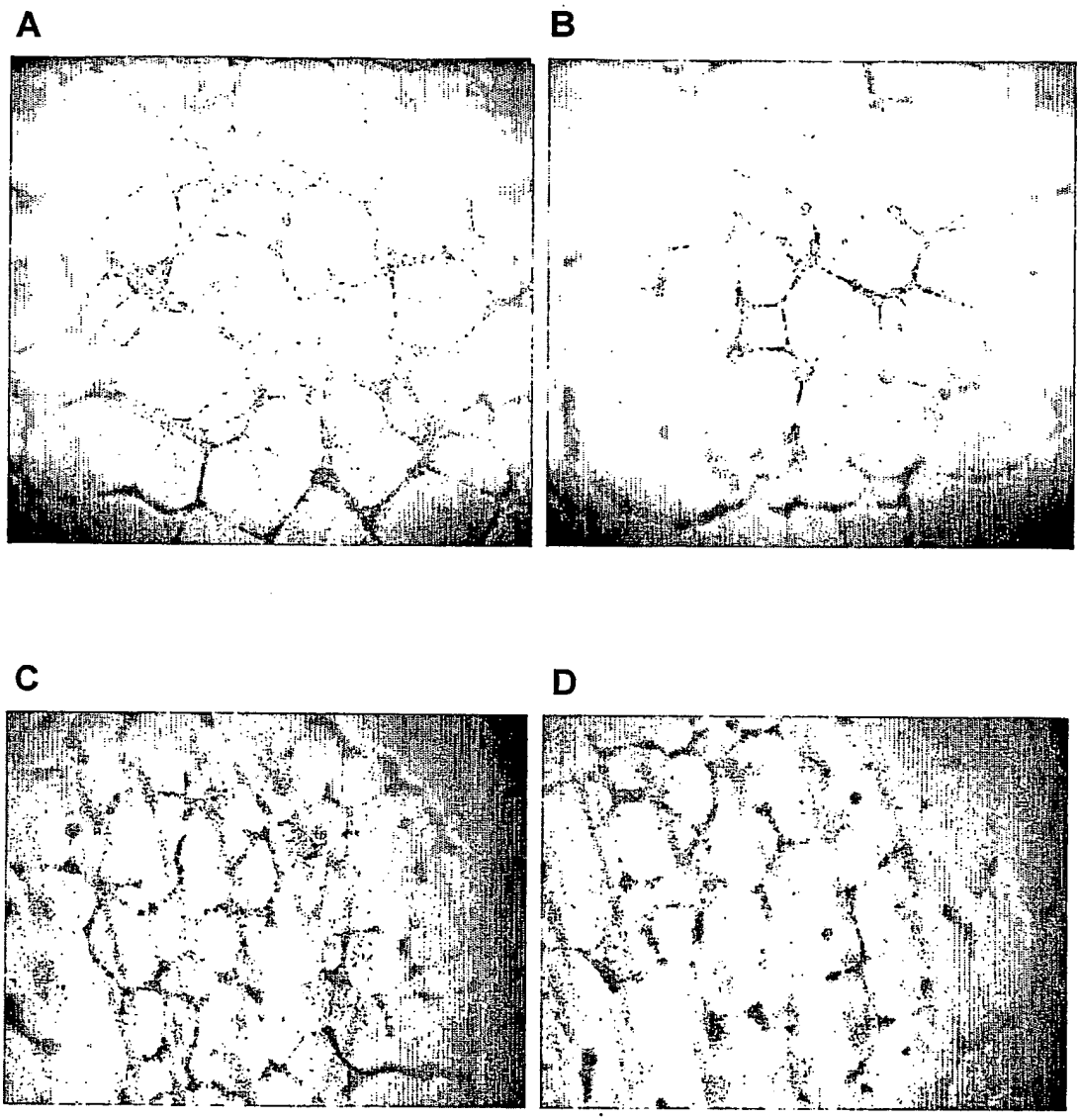

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398

<210> 21
<211> 443
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<400> 21
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taaactcttt aaagaaccag cttttgattt ccttgatttc tgttctgatc tttattactc
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<210> 22
<211> 385
<212> DNA
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<400> 22

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<210> 23
<211> 1014
<212> DNA
<213> Homo sapiens

<400> 23
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atgtaacata tggggtattc taagcccttt gcacgcccaa ttcaggaaat ccaactgctg
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420

caaaaaagtg tttctccgaa ttttcaagat tagttcctat atctgtgcta ctgatagccc
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900

caataaaata taatctacaa atttcagtaa aatacaatcc aaaaaatccc tccctttcc
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1014

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<212> DNA
<213> Homo sapiens

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gatttcaatc aagattgatc aaaacctgat gaaaatatcc tgataatcaa tgggaagtag
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<210> 25
<211> 248
<212> DNA
<213> Homo sapiens

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248

<210> 26
<211> 1132
<212> DNA
<213> Homo sapiens

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caatacactc ccttaatggg tgttattatt ccattgtaat gaaataatat tccatggtag
420

cagaaggaat gcttaaattc tgccttactg ttaaattcta tatagatact tgggttggtc
480

aaattaattt ggtgcttcac ccaaagcccc aatgtatttg aactttaatc tttcatagga
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600

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720

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960

acaaaaaaaa aattctaaaa atcaaaaaaa cttcctaatc ctgaaaaagt aaaattaatt
1020

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1080

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1132

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<211> 646
<212> DNA
<213> Homo sapiens

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caagtcccac atagctggct gattactgag ctttgagcag gtagcactgg tcactatgca
180

cagattagta tgattactga gctttgagca gcttgaacag atcactatga tataggctct
240

ggaaaggttg tgcagatatg cctgatgcca aggcactggc aaaattgttg gtaggctggc
300

aagttagttc cttctcaagg aaaaaaaagt gtgaatgatc ctataggtta ctagacagac
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atgcagtttc cctttggaga aggttgactt tggactttga gaaatacatt ttttttcttt
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<211> 417
<212> DNA
<213> Homo sapiens

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gagtatgcat gtgctgttat ttattttaaa cattatcttt ttttctccct gtcttgacag
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aataaccatc aaggatgatg taattacaaa actcaagatg atttgacaga atttttcaaa
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<210> 30
<211> 291
<212> DNA
<213> Homo sapiens

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gcttaagtgt tacttctctg tattaaagct tcaagttcac tcactgtcta accaatgata
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cacagctacc tgaagacatt aaaatctttc ataaatttat tctcaatttt tttcttctta
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<210> 31
<211> 1154
<212> DNA
<213> Homo sapiens

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aaaccactaa ttaaacactt ttgtttctct ttttttaag ccattaatac tgatacctag
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agagaaaaat aaaaaccaga aatactttca aaagccaagc atgatagact agcatttatc
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ccaaaacact aagaaattac aaaactcaat agcaaaataa ctcacgtgtt acaaccataa
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420

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<211> 875
<212> DNA
<213> Homo sapiens

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420

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<210> 33
<211> 1270
<212> DNA
<213> Homo sapiens

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tagctaccac agctagtctc tcacatgaca gataagatga atggatagcg catcaatggt
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tgacaacttc tctaaagtaa atacgcgctg gctgtctctt ttcaagatta acacaagata
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420

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480

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720

gaaccccacc gctatcaccc tcccgctttg acgcggtgca caaccgcccc ccgcgctcca
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<210> 34
<211> 501
<212> DNA
<213> Homo sapiens

<400> 34
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acccacatcc cactttcctt tactgcagaa attgacaagc tgatccaaaa aattgtaagg
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aaatggcaag ggatccataa tagacaaaac aattttgaaa aagaataaaa tcaaagggct
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atagagatat tgaacttcat caaaattaaa aacttttgca tttcaactat caaaaaaaaa
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<210> 35
<211> 373
<212> DNA
<213> Homo sapiens

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<210> 36
<211> 563
<212> DNA

<213> Homo sapiens

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<210> 37
<211> 1280
<212> DNA
<213> Homo sapiens

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1280

<210> 38
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<212> DNA
<213> Homo sapiens

<400> 38
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aaaaaatatt gattggataa ttaaaaagag attttggtga tggggatgaa gatctatata
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cgggagtgtt gtatgcttcc cccttgacgc cagtgcaaaa acctagatcc taggccccta
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attaactgca acgaagacat cctacacgtc cctgttatac atcattccac acaaattttc
720

gtcccccaac tacctatgat ttcccctaac attacctcaa actatcgtct ctacaactga
780

ggagtaatac cacccgtaca acgtcacaag aatggctaat ttctaaaaca tgcgatagcc
840

tgcgatagac tagaatacac aattcatcta caaaaaaaat ctgacccaat gaaattaata

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<212> DNA
<213> Homo sapiens

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120

ttatgcatct ataacaagtc ccacatagct ggctgattac tgagctttga gcaggtagca
180

ctggtcacta tgcacagatt agtatgatta ctgagctttg agcagcttga acagatcact
240

atgatatagg ctctggaaag gttgtgcaga tatgcctgat gccaaggcac tggcaaaatt
300

gttggtaggc tggcaagtta gttccttctc aaggaaaaaa aagtgtgaat gatcctatag
360

gttactagac agacatgcag tttccctttg gagaaggttg actttggact ttgagaaata
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catttttttt cttttaatct aaagagattt gaaaataata gatgtccaat ttttgtttac
480

ctattctgaa ctataaggca cattgctttg ttcttctgtg cctcagttta ccccttttag
540

taaaggaggt ctattttaat cagtgagagc ttcaggtagc tggaggaatg cttcaggaaa
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<210> 40
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<212> DNA
<213> Homo sapiens

<400> 40

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120

actagctgag atagacgact atacaacaac taaagaaaaa gaaaaaatat tataatatct
180

catgtatcta gtgttacaga gaagttccca tcaactgctg catcagttag ttaactggag
240

gaataacacg aactatgaat agatgaccat tttttcagag aagtagaata aaataaaatt
300

caccaaatac aataaaataa gtaatatttt taaaataagt agcataaaat ataataaaat
360

tcagatagag aaaatgaaca gggttcaatt ttttttctga tgtcaagtta ccatttgttt
420

cctattcatg gagttgaagt gactaaactt tttgataatg ccagatttat tcataattcc
480

tggataaagg aatttaatga aaaaaatata atgactagta tatttctaag gccataaaac
540

tgtcccaaag aaataaactg aaaaagtgag aaaattaggt tcaccaatct gcatgtatat
600

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<212> DNA
<213> Homo sapiens

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120

caactactct gtcttgagct caaatgggac aggcatactc ttcagcatag ccatcgtaca
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attgctcttc tcgagctact atcacccaca ttaaggtctt tcatgtcctg atttagacgc
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gagctctgtg cctagcgagg ttattcctac ccctgttgta cgtgcccggg cggacggtca
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tgatcatggg catgagacgg gctgatggaa ggctggatct agcaaaatcc tggcgtcaaa
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420

gttggctatt atactgtcct tgagatcaca tataacagac ctatctcaag gctgtgaaaa
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aagtccttta acacgatcaa attatctgtg tagcagacat atatatcaag cagtatagaa
540

actacttaca catgcaattt acagatatct ctagggaaaa aacaagcact cacgaatagc
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attatacatt aggtagagac tcttgatatg tctgttaact agatgatttt ccaaatatat
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catttgtcct atgggaagct gaattaaggt aggaaaatac tttttgctac attgctattt
180

ggggaaacgc tctgatagaa ggtctccata gttggtggaa ttccagaatc caattagcac
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ccgaatgaaa tgtaaataat aggtctcaca attttatgtc agatgtgctg tgtatgagcc
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cagacatatt ttcacaaatt agttgtccta atgctggttt tattttggtg tattataatt
360

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420

cacagtgatg tgtattgaat aaatgaatac atgaatgaat aaacctcttg atcactgccc
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540

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572

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<213> Homo sapiens

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120

tggctagggg cagtgttatc ctgttcataa atcaggtgtt ctcagagatt taataattta
180

gaattcacat gaggatttgg tggaataaac atttcctttc tctgttaagc tgcctcttaa
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120

agtcttctaa gattatagct ttaaaatgac taatttaggg tattagatat gccaagttct
180

atgaagagtt cccttgtaat taaactccac aaaaagtaaa ttcaattgta tttaaaatgc
240

cttccattta tccctttttag taaactaatt ctgacattcc cagaagttgt ctaaaaattt
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gcttctcagt ctatgtaagc ggtaaacata tttttctgga acaaaggtga ttgaagctag
360

tctgaactaa tcattagcaa gtttgctaaa ataaggttaa gagggaaaac tctctattcc
420

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<210> 51
<211> 64
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<400> 51

Gln Val Leu Glu Val Tyr Ser Leu Phe Gly Leu Leu Ser Asn Phe Asn
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His Lys Ile Gln Asn Val Asn Tyr Gln His His Phe Ala Tyr Tyr Ala
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Phe Cys Thr Leu Ile Ala Ala Thr Ser Lys Asn Arg Thr Lys Gly Pro
35 40 45

Phe Phe Gly Thr Ile Ser His Phe Thr Thr Lys Lys Gln Tyr Gln Glu
50 55 60

<210> 52
<211> 63
<212> PRT
<213> Homo sapiens

<400> 52

Leu Asp Ser Val Ala Glu Asn Thr Tyr Arg Val Leu Ser Ser Ile Pro
1 5 10 15

Phe Phe Cys Pro Pro Lys Lys Ala Gly Leu Tyr Ala Glu Ser Pro Lys
20 25 30

Thr Lys Gln Lys Thr Pro Ser Asn Ile Gln Ile Phe Asn Asn Val Ile
35 40 45

Lys Asn Phe Met Ile Pro Lys Gly Phe Val Cys Ala Leu Ala Met
50 55 60

<210> 53
<211> 42
<212> PRT
<213> Homo sapiens

<400> 53

Gly Thr Leu Phe Leu Arg Val Gly Phe Leu Leu Phe Leu Phe Phe Tyr
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Ser Phe Ile Tyr Ile Gln Ile Gly Glu Pro Asn Phe Leu Thr Phe Ser
20 25 30

Val Tyr Phe Phe Gly Thr Val Leu Trp Pro
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<210> 54
<211> 98
<212> PRT
<213> Homo sapiens

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Met Asp Gln Arg Leu Gly His Cys Gln Leu Ser Ala His Ile Leu His

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Ile Thr His Leu Gln Val Leu Lys Thr Gly Lys Cys Pro Gly Ala Gly
20 25 30

Arg Cys Cys Lys His Val Ser Val Pro Gly Gly Gly Ala Pro Ala Gln
35 40 45

Leu Ile Gly Asp Ser Phe Tyr Pro Ala His Pro Phe Gly Gly Tyr Thr
50 55 60

Ser Leu Ala Gln Ser Leu Ile Ala Glu Glu His Pro Pro Ala Asn Ser
65 70 75 80

Ala Gln Ser Pro Pro Pro Val Leu Thr Thr Phe His Trp Phe Val Cys
85 90 95

Leu Asn

<210> 55
<211> 62
<212> PRT
<213> Homo sapiens

<400> 55

Ala Ala Pro Gly Ala Val Pro Arg Ser Arg Leu Phe Glu Val Arg Ser
1 5 10 15

Ala Leu Ser Val Ala Lys Gln Ile Thr Ala Ser Thr Leu Leu Ser Val
20 25 30

Phe Ser Phe Val Val Leu Thr Ser Val Ala His Leu Asp Leu Gly Cys
35 40 45

Tyr Tyr Ile Phe Val Phe Ile Ile Asn Ser Cys Thr Cys Phe
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<210> 56
<211> 52

<212> PRT
<213> Homo sapiens

<400> 56

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1 5 10 15

Ile Gln Asn Leu Ile Tyr Phe Trp Ser Arg Ala Phe Gln Ile Arg Asp
20 25 30

Thr Gln His Val Phe Val Thr Phe Asn Thr Asn Glu Ile Ser Lys Phe
35 40 45

Cys Phe Leu His
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<210> 57
<211> 33
<212> PRT
<213> Homo sapiens

<400> 57

Ile Asp Arg Asn Ile Asn Thr His Glu Arg Glu Asp Asn Glu Arg Phe
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Val Ser Phe Val Cys His Lys Ser Thr Phe Phe Asn His Ser Leu Leu
20 25 30

Val

<210> 58
<211> 103
<212> PRT
<213> Homo sapiens

<400> 58

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Gly Trp Thr Leu Ala Pro Lys Ala Tyr Arg Thr Leu Asn Pro Pro Asp

20 25 30

Ala Pro Ala Cys Leu His Leu Ser Pro Ile Leu Arg Ala Pro Pro Pro
35 40 45

Thr Leu Ser Ser Ile Ala Asn Pro Leu Ile Leu Ile Asp Gly Ala Phe
50 55 60

Asn Pro Leu Cys Gly Pro Pro Arg Pro Ser Leu Glu Ile Thr Gly Phe
65 70 75 80

His Pro Pro Ile Pro Phe Pro His Thr Leu His Gly Ala Gly Ser Pro
85 90 95

Arg Pro Pro Phe Leu His Ser
100

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000383

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. [7]: C12Q 1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
SEE BELOW

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
SEE BELOW

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WPIDS, BIOSIS, MEDLINE, CAPLUS: Suppression subtractive hybridisation/hybridization, angiogen?, time/stage

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO 2003/027285 A1 (Bionomics Ltd) 3 April 2003 Example 3	1, 2, 5, 6
X	WO 1996/023079 A2 (Clontech Laboratories Inc) 1 August 1996 p. 17 line 11 - p. 18 line 21	1, 2, 5, 6
X	Diatchenko, L. et al., 1996, Suppression subtractive hybridization: a method for genereating differentially regulated or tissue specific cDNA probes and libraries, ***Proceedings of the National Academy of Sciences USA***, 93:6025-6030 Whole document	1, 2, 5, 6

[X] Further documents are listed in the continuation of Box C [X] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 July 2004	14 JUL 2004
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. (02) 6285 3929	Authorized officer **JAMIE TURNER** Telephone No : (02) 6283 2071

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000383

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Glienke, J. et al., 2000, Differential gene expression by endothelial cells in distinct angiogenic states, ***European Journal of Biochemistry***, 267:2820-2830. Whole document	1, 2, 5, 6

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000383

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: **3, 4, 7-9**
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

See Supplemental Box

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See Supplemental Box

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: **1-9**

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000383

Supplemental Box

Continuation of Box No II (Observations where certain claims were found unsearchable):

Claims 3, 4, 7-9 are not limited to the technical features of the invention because the claims are not limited to nucleic acid molecules or polypeptides that could only have been produced using the applicant's invention.

The applicant's invention resides in a method for the identification of a nucleic acid molecule differentially expressed in an *in vitro* model of a biological system by performing suppression subtractive hybridisation on cDNA pools from distinct time points sequentially so as to amplify cDNAs derived from nucleic acid molecules differentially expressed from one time point to the the next.

Claims 3, 4, 7-9 define a nucleic acid molecule ***when identified*** by the method of the invention, and the polypeptide encoded by these nucleic acid molecules. However, a method of identification does not produce a product, it merely provides new information about a pre-existing compound. As such the claim simply defines a compound *per se*, not a product of the applicant's invention, hence the claims are not limited to the technical features of the invention.

Continuation of Box No III (Observations where unity of invention is lacking):

The International Searching Authority has found that there are different inventions as follows:

Invention 1: Claims 1-9 (completely) relating to a method for the identification of a nucleic acid molecule differentially expressed in an *in vitro* model of a biological system, comprising the step of performing a suppression subtractive hybridisation using cDNA isolated at different time points, wherein the cDNA pools from the different time points are subtracted sequentially so as to progressively amplify the nucleic acid molecules differentially expressed from one time period to the next.

Inventions 2-45: Claims 10, 17-21, 27, 34, 36, 54, 56, 76, 78, 109-115 (completely), and 11-16, 22-26, 28-33, 35, 37-53, 55, 57-75, 77, 79-108, 116-136 (partially). These claims relate to a nucleic acid molecule comprising the sequence set forth in one of SEQ ID NO: 1-44, the encoded polypeptide, antibodies reactive with the isolated polypeptide, siRNA/DNAzymes and ribozymes that target to SEQ ID NO: 1-44, and various methods that make use of said nucleic acid molecules and/or polypeptides, antagonists or agonists of said nucleic acid molecules or antibodies that bind the encoded polypeptide.

Each of the 44 genes set forth in SEQ ID NO:1-44 represent a distinct invention.

Inventions 46-516: Claims 11-16, 22-26, 28-33, 35, 37-53, 55, 57-75, 77, 79-108, 116-136 (partially) with respect to each of the 471 additional genes set forth in Tables 1 and 2, and methods that make use of said nucleic acid molecules and/or polypeptides, antagonists or agonists of said nucleic acid molecules or antibodies that bind the encoded polypeptide.

Each of the 471 genes set forth in Tables 1 and 2 is considered a distinct invention.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/AU2004/000383

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member					
WO	1996/023079	AU	47741/96	EP	0753075	US	5565340
		US	5759822				
WO	2003/027285	CA	2461372	EP	1430126		

Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.

END OF ANNEX